

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
7 December 2000 (07.12.2000)

PCT

(10) International Publication Number  
**WO 00/73468 A1**

(51) International Patent Classification<sup>7</sup>: C12N 15/54,  
15/11, 15/63, 9/12, 1/21, 5/10, 15/09, C07K 16/40, C12Q  
1/48

(74) Agent: SPRUNGER, Suzanne, A.; 51 University Street,  
Seattle, WA 98101 (US).

(21) International Application Number: PCT/US00/14696

(22) International Filing Date: 26 May 2000 (26.05.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
60/136,781 28 May 1999 (28.05.1999) US

(71) Applicant (for all designated States except US): IM-  
MUNEX CORPORATION [US/US]; 51 University  
Street, Seattle, WA 98101 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): BIRD, Timothy,  
A. [US/US]; 10804 Olallie Drive NE, Bainbridge Island,  
WA 98110 (US). VIRCA, G., Duke [US/US]; 16690 SE  
50th Place, Bellevue, WA 98006 (US). MARTIN, Unja  
[US/US]; 928 NW 64th Street, Seattle, WA 98107 (US).  
ANDERSON, Dirk, M. [US/US]; 3616 NW 64th Street,  
Seattle, WA 98107 (US).

(81) Designated States (*national*): AE, AL, AM, AT, AU, AZ,  
BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK,  
DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,  
IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,  
LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT,  
RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA,  
UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian  
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European  
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,  
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

**Published:**

- With international search report.
- Before the expiration of the time limit for amending the  
claims and to be republished in the event of receipt of  
amendments.

For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.

(54) Title: NOVEL MURINE AND HUMAN KINASES

(57) Abstract: The invention is directed to purified and isolated novel murine and human kinase polypeptides, the nucleic acids encoding such polypeptides, processes for production of recombinant forms of such polypeptides, antibodies generated against these polypeptides, fragmented peptides derived from these polypeptides, and the uses of the above.



WO 00/73468 A1

## NOVEL MURINE AND HUMAN KINASES

5

This application claims the priority of provisional application U.S. Serial No. 60/136,781, filed May 28, 1999, which is incorporated by reference herein.

### BACKGROUND OF THE INVENTION

#### 10 Field of the Invention

The invention is directed to purified and isolated novel murine and human kinase polypeptides and fragments thereof, the nucleic acids encoding such polypeptides, processes for production of recombinant forms of such polypeptides, fragmented peptides derived from these polypeptides, antibodies generated against these polypeptides, methods of identifying  
15 activators and inhibitors of the activity of these kinases, and therapeutic and diagnostic uses thereof.

#### Background

Cells respond to external signals and internal signals, such as those produced by  
20 disease conditions, by activating cellular signaling pathways. Cellular signaling often involves a molecular activation cascade, during which a receptor propagates a ligand-receptor mediated signal by specifically activating intracellular protein kinases which phosphorylate target substrates. These substrates can themselves be kinases which become activated following phosphorylation.

25 The eukaryotic protein kinases make up a large and rapidly expanding family of proteins related on the basis of homologous catalytic domains. Spurred by the development of gene cloning and sequencing methodologies, distinct protein kinase genes have been identified from a wide selection of invertebrates and lower eukaryotes, including *Drosophila*, *Caenorhabditis elegans*, *Aplysia*, *Hydra*, *Dictyostelium*, and budding (*Saccharomyces cerevisiae*) and fission (*Schizosaccharomyces pombe*) yeast. Homologous genes have also  
30 been identified in higher plants. Protein kinases, however, are not limited to the eukaryotes.

Enzyme activities have been well documented in prokaryotes, but the prokaryotic protein kinase genes are not obviously similar to those of the eukaryotes.

Given the important function of kinases in general, there is a need in the art for additional members of the kinase family. In addition, in view of the continuing interest in protein research, the discovery, identification, and roles of new proteins, such as protein kinases, are at the forefront of modern molecular biology and biochemistry. Despite the growing body of knowledge, there is still a need in the art for the identity and function of proteins having kinase activities. In addition, because there is an unmet need for therapeutic compounds which modulate kinase activity and because protein kinases are useful biochemical reagents, there is also need in the art for the continued discovery of unique members of the protein kinase family and potential therapeutic targets thereof.

#### **SUMMARY OF THE INVENTION**

The invention aids in fulfilling these various needs in the art by providing isolated murine and human kinase nucleic acids and polypeptides encoded by these nucleic acids. Particular embodiments of the invention are directed to isolated murine and human kinase nucleic acid molecules comprising the DNA sequences of SEQ ID NOs:1-7 and isolated murine and human kinase nucleic acid molecules encoding the amino acid sequences of SEQ ID NOs:8-14, as well as nucleic acid molecules complementary to these sequences. Both single-stranded and double-stranded RNA and DNA nucleic acid molecules are encompassed by the invention, as well as nucleic acid molecules that hybridize to a denatured, double-stranded DNA comprising all or a portion of SEQ ID NOs:1-7. Also encompassed are isolated nucleic acid molecules that are derived by *in vitro* mutagenesis of nucleic acid molecules comprising sequences of SEQ ID NOs:1-7, that are degenerate from nucleic acid molecules comprising sequences of SEQ ID NOs:1-7, and that are allelic variants of DNA of the invention. The invention also encompasses recombinant vectors that direct the expression of these nucleic acid molecules and host cells stably or transiently transformed or transfected with these vectors.

In addition, the invention encompasses methods of using the nucleic acids noted above to identify nucleic acids encoding proteins having kinase activity and to study cell signal transduction.

The invention also encompasses the use of sense or antisense oligonucleotides from the nucleic acid of SEQ ID NOs:1-7 to inhibit the expression of the polynucleotide encoded by the kinase genes.

5 The invention also encompasses isolated polypeptides and fragments thereof encoded by these nucleic acid molecules including soluble polypeptide portions of SEQ ID NOs:8-14. The invention further encompasses methods for the production of these polypeptides, including culturing a host cell under conditions promoting expression and recovering the polypeptide from the culture medium. Especially, the expression of these polypeptides in bacteria, yeast, plant, insect, and animal cells is encompassed by the invention.

10 In general, the polypeptides of the invention can be used to study cellular processes such as signal transduction and to screen for compounds which modulate kinase activity which may have therapeutic potential. In addition, these polypeptides can be used to identify proteins associated with the polypeptides of the invention.

15 In addition, the invention includes assays utilizing these polypeptides to screen for potential inhibitors of activity associated with polypeptide counter-structure molecules, and methods of using these inhibitors as therapeutic agents for the treatment of cancer and other proliferative diseases and diseases mediated by polypeptide counter-structure molecules. Further, methods of using these polypeptides in the design of inhibitors thereof are also an aspect of the invention.

20 The invention further provides a method for using these polypeptides as molecular weight markers that allow the estimation of the molecular weight of a protein or a fragmented protein, as well as a method for the visualization of the molecular weight markers of the invention thereof using electrophoresis. The invention further encompasses methods for using the polypeptides of the invention as markers for determining the isoelectric point of an unknown protein, as well as controls for establishing the extent of fragmentation of a protein.

25 Further encompassed by this invention are kits to aid in these determinations.

Further encompassed by this invention is the use of the kinase nucleic acid sequences, predicted amino acid sequences of the polypeptide or fragments thereof, or a combination of the predicted amino acid sequences of the polypeptide and fragments thereof for use in  
30 searching an electronic database to aid in the identification of sample nucleic acids and/or proteins.

Isolated polyclonal or monoclonal antibodies that bind to these polypeptides are also encompassed by the invention, in addition the use of these antibodies to aid in purifying the murine and human kinase polypeptides.

Also encompassed by the invention is a method of designing an inhibitor of the  
5 kinase polypeptide of the invention, the method comprising the steps of determining the three-dimensional structure of such polypeptide, analyzing the three-dimensional structure for the likely binding sites of substrates, synthesizing a molecule that incorporates a predicted reactive site, and determining the polypeptide-inhibiting activity of the molecule.

Another aspect of the invention is a method for identifying compounds that activate  
10 or inhibit kinase activity comprising:

- (a) bringing a test compound into contact with the polypeptide of the invention and a substrate; and
- (b) determining whether the test compound activates or inhibits the kinase activity of said polypeptide. In a preferred embodiment of this method, the test compound  
15 is brought into contact with the polypeptide in a cell containing at least one recombinant vector that directs the expression of at least one polynucleotide encoding said polypeptide.

Another aspect of the invention is a method for inhibiting the kinase activity of the polypeptide of the invention comprising forming a mixture of the polypeptide, a substrate, and a compound, wherein the compound blocks the binding of the polypeptide with the  
20 substrate.

### **BRIEF DESCRIPTION OF THE FIGURES**

Figures 1-6 each depict an alignment of the amino acid sequence of a kinase of the invention (top line) with the conserved amino acid residues of the family of protein  
25 serine/threonine kinases (bottom line). Invariant residues are shown in UPPER CASE letters, nearly-invariant residues as lower case, conserved hydrophobic residues as (o), conserved polar residues as (\*), and conserved small residues with near neutral polarity as (+).

Figure 1 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MDCK-1.

30 Figure 2 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MDCK-2.

Figure 3 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MDCK-3.

Figure 4 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MLSK-1.

5 Figure 5 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with MLSK-2.

Figure 6 presents the amino acid sequence alignment of the consensus protein serine/threonine kinase sequence with LNRK-1.

10

### **DETAILED DESCRIPTION OF THE INVENTION**

The molecules encompassed in the invention include the following nucleotide and amino acid sequences:

Kinase:	DNA Sequence:	Protein Sequence:
MDCK-1	SEQ ID NO:1	SEQ ID NO:8
MDCK-2	SEQ ID NO:2	SEQ ID NO:9
MDCK-3	SEQ ID NO:3	SEQ ID NO:10
MLSK-1	SEQ ID NO:4	SEQ ID NO:11
MLSK-2	SEQ ID NO:5	SEQ ID NO:12
ss4694	SEQ ID NO:6	SEQ ID NO:13
LNRK-1	SEQ ID NO:7	SEQ ID NO:14
LNRK-1 primers	SEQ ID NO:15 and SEQ ID NO:16	

15

The discovery of the nucleic acids of the invention enables the construction of expression vectors comprising nucleic acid sequences encoding polypeptides; host cells transfected or transformed with the expression vectors; isolated and purified biologically active polypeptides and fragments thereof; the use of the nucleic acids or oligonucleotides thereof as probes to identify nucleic acid encoding proteins having kinase activity; the use

20

of single-stranded sense or antisense oligonucleotides from the nucleic acids to inhibit expression of polynucleotides encoded by the kinase genes of the invention; the use of such polypeptides and soluble fragments to function as kinases; the use of such polypeptides and

fragmented peptides as molecular weight markers; the use of such polypeptides and fragmented peptides as controls for peptide fragmentation, and kits comprising these reagents; the use of such polypeptides and fragments thereof to generate antibodies; and the use of antibodies to purify the human and murine kinase polypeptides.

5

#### NUCLEIC ACID MOLECULES

In a particular embodiment, the invention relates to certain isolated nucleotide sequences that are free from contaminating endogenous material. A "nucleotide sequence" refers to a polynucleotide molecule in the form of a separate fragment or as a component of  
10 a larger nucleic acid construct. The nucleic acid molecule has been derived from DNA or RNA isolated at least once in substantially pure form and in a quantity or concentration enabling identification, manipulation, and recovery of its component nucleotide sequences by standard biochemical methods (such as those outlined in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd sed., Cold Spring Harbor Laboratory, Cold Spring  
15 Harbor, NY (1989)). Such sequences are preferably provided and/or constructed in the form of an open reading frame uninterrupted by internal non-translated sequences, or introns, that are typically present in eukaryotic genes. Sequences of non-translated DNA can be present 5' or 3' from an open reading frame, where the same do not interfere with manipulation or expression of the coding region.

20 Nucleic acid molecules of the invention include DNA in both single-stranded and double-stranded form, as well as the RNA complement thereof. DNA includes, for example, cDNA, genomic DNA, chemically synthesized DNA, DNA amplified by PCR, and combinations thereof. Genomic DNA may be isolated by conventional techniques, e.g., using the cDNA of SEQ ID NOs:1-7, or a suitable fragment thereof, as a probe.

25 The DNA molecules of the invention include full length genes as well as polynucleotides and fragments thereof. Other embodiments include DNA encoding a soluble form of the protein.

The nucleic acids of the invention are preferentially derived from murine and human sources, but the invention includes those derived from other sources, as well.

30

### Preferred Sequences

Particularly preferred nucleotide sequences of the invention are SEQ ID NOs:1-7, as set forth above. The sequences set forth in SEQ ID NOs:1-3 are Murine Dendritic Cell Kinases (MDCK) 1 to 3, respectively. SEQ ID NOs:4-5 are Murine Lymph node Stomal cell Kinases (MLSK) 1 and 2. Finally, SEQ ID NO:6 is from human dendritic cells and is called SS-4694. This sequence was utilized to clone full length SEQ ID NO:7, called Large NIK-Related Kinase (LNRK) 1.

Clones having the nucleotide sequences of SEQ ID NOs:1-7 were isolated as described in Example 1. The sequences of amino acids encoded by the DNAs of SEQ ID NOs:1-7 are shown in SEQ ID NOs:8-14. As set forth in detail below, the amino acid sequences for MDCK-1 (SEQ ID NO:8), MDCK-2 (SEQ ID NO:9), MDCK-3 (SEQ ID NO:10), MLSK-1 (SEQ ID NO:11), MLSK-2 (SEQ ID NO:12), ss4694 (SEQ ID NO:13), and LNRK-1 (SEQ ID NO:14) identify the polynucleotides as a member of the kinase superfamily.

Particularly preferred polynucleotides that encode the kinases of the invention and which comprise certain nucleotide sequences of SEQ ID NOs:1-7 are as follows:

- nucleotides 71-893 of SEQ ID NO:1 (MDCK-1);
- nucleotides 115-1020, 136-1020, and 190-1020 of SEQ ID NO:2 (MDCK-2);
- nucleotides 243-1307 of SEQ ID NO:3 (MDCK-3);
- nucleotides 123-2015 of SEQ ID NO:4 (MLSK-1);
- nucleotides 121-1053 of SEQ ID NO:5 (MLSK-2);
- nucleotides 95-892 of SEQ ID NO:6 (ss4694); and
- nucleotides 1-4080 of SEQ ID NO:7 (LNRK-1).

### Additional Sequences

Due to the known degeneracy of the genetic code, wherein more than one codon can encode the same amino acid, a DNA sequence can vary from that shown in SEQ ID NOs:1-7 and still encode a polypeptide having the amino acid sequence of SEQ ID NOs:8-14. Such variant DNA sequences can result from silent mutations (*e.g.*, occurring during PCR amplification), or can be the product of deliberate mutagenesis of a native sequence.

The invention thus provides isolated DNA sequences encoding polypeptides of the invention, selected from: (a) DNAs comprising the nucleotide sequence of SEQ ID NOs:1-7;



(b) DNAs encoding the polypeptides of SEQ ID NOs:8-14; (c) DNA capable of hybridization to a DNA of (a) or (b) under conditions of moderate stringency and which encodes polypeptides of the invention; (d) DNA capable of hybridization to a DNA of (a) or (b) under conditions of high stringency and which encodes polypeptides of the invention, and (e) DNA  
5 which is degenerate as a result of the genetic code to a DNA defined in (a), (b), (c), or (d) and which encode polypeptides of the invention. Of course, polypeptides encoded by such DNA sequences are encompassed by the invention.

As used herein, conditions of moderate stringency can be readily determined by those having ordinary skill in the art based on, for example, the length of the DNA. The basic  
10 conditions are set forth by Sambrook et al. *Molecular Cloning: A Laboratory Manual*, 2 ed. Vol. 1, pp. 1.101-104, Cold Spring Harbor Laboratory Press, (1989), and include use of a prewashing solution for the nitrocellulose filters 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0), hybridization conditions of about 50% formamide, 6X SSC at about 42°C (or other similar hybridization solution, such as Stark's solution, in about 50% formamide at about  
15 42°C), and washing conditions of about 60°C, 0.5X SSC, 0.1% SDS. Conditions of high stringency can also be readily determined by the skilled artisan based on, for example, the length of the DNA. Generally, such conditions are defined as hybridization conditions as above, and with washing at approximately 68°C, 0.2X SSC, 0.1% SDS. The skilled artisan will recognize that the temperature and wash solution salt concentration can be adjusted as  
20 necessary according to factors such as the length of the probe. Preferred hybridizing polynucleotides are those that are at least 25%, more preferably 50%, and most preferably 75% of the length of the polynucleotide to which they hybridize.

Also included as an embodiment of the invention is DNA encoding polypeptide fragments and polypeptides comprising inactivated N-glycosylation site(s), inactivated  
25 protease processing site(s), or conservative amino acid substitution(s), as described below.

In another embodiment, the nucleic acid molecules of the invention also comprise nucleotide sequences that are at least 80% identical to a native sequence. Also contemplated are embodiments in which a nucleic acid molecule comprises a sequence that is at least 90% identical, at least 95% identical, at least 98% identical, at least 99% identical, or at least  
30 99.9% identical to a native sequence.

The percent identity may be determined by visual inspection and mathematical calculation. Alternatively, the percent identity of two nucleic acid sequences can be

determined by comparing sequence information using the GAP computer program, version 6.0 described by Devereux et al. (*Nucl. Acids Res.* 12:387, 1984) and available from the University of Wisconsin Genetics Computer Group (UWGCG). The preferred default parameters for the GAP program include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) for nucleotides, and the weighted comparison matrix of Gribskov and Burgess, *Nucl. Acids Res.* 14:6745, 1986, as described by Schwartz and Dayhoff, eds., *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, pp. 353-358, 1979; (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps. Other programs used by one skilled in the art of sequence comparison may also be used.

The invention also provides isolated nucleic acids useful in the production of polypeptides. Such polypeptides may be prepared by any of a number of conventional techniques. A DNA sequence encoding a kinase polypeptide of the invention, or desired fragment thereof, may be subcloned into an expression vector for production of the polypeptide or fragment. The DNA sequence advantageously is fused to a sequence encoding a suitable leader or signal peptide. Alternatively, the desired fragment may be chemically synthesized using known techniques. DNA fragments also may be produced by restriction endonuclease digestion of a full length cloned DNA sequence, and isolated by electrophoresis on agarose gels. If necessary, oligonucleotides that reconstruct the 5' or 3' terminus to a desired point may be ligated to a DNA fragment generated by restriction enzyme digestion. Such oligonucleotides may additionally contain a restriction endonuclease cleavage site upstream of the desired coding sequence, and position an initiation codon (ATG) at the N-terminus of the coding sequence.

The well-known polymerase chain reaction (PCR) procedure also may be employed to isolate and amplify a DNA sequence encoding a desired protein fragment. Oligonucleotides that define the desired termini of the DNA fragment are employed as 5' and 3' primers. The oligonucleotides may additionally contain recognition sites for restriction endonucleases, to facilitate insertion of the amplified DNA fragment into an expression vector. PCR techniques are described in Saiki et al., *Science* 239:487 (1988); *Recombinant DNA Methodology*, Wu et al., eds., Academic Press, Inc., San Diego (1989), pp. 189-196; and *PCR Protocols: A Guide to Methods and Applications*, Innis et al., eds., Academic Press, Inc. (1990).

POLYPEPTIDES AND FRAGMENTS THEREOF

The invention encompasses polypeptides and fragments thereof in various forms, including those that are naturally occurring or produced through various techniques such as procedures involving recombinant DNA technology. Such forms include, but are not limited to, derivatives, variants, and oligomers, as well as fusion proteins or fragments thereof.

Polypeptides and Fragments Thereof

The polypeptides of the invention include full length proteins encoded by the nucleic acid sequences set forth above. Particularly preferred polypeptides comprise the amino acid sequences of SEQ ID NOs:8-14 as follows:

- amino acids 1-275, 25-275, 140-226, and 149-175 of SEQ ID NO:8 (MDCK-1);
- amino acids 1-302, 8-302, 26-302, 34-295, 60-229, 157-183, and 198-229 of SEQ ID NO:9 (MDCK-2);
- amino acids 1-355, 23-279, 124-221, 134-169, and 183-214 of SEQ ID NO:10 (MDCK-3);
- amino acids 1-631, 57-309, 129-254, 175-200, and 215-247 of SEQ ID NO:11 (MLSK-1);
- amino acids 1-311, 14-271, 41-213, 124-161, and 175-206 of SEQ ID NO:12 (MLSK-2);
- amino acids 1-266, 1-261, 25-258, 101-233, 149-175, and 190-226 of SEQ ID NO:13 (ss4694); and
- amino acids 1-1360, 25-306, 25-258, 101-233, 149-175, and 190-226 of SEQ ID NO:14 (LNRK-1).

As set forth in Figures 1-6, alignments of the polypeptide sequences of the invention (SEQ ID NOs:8-12 and 14) with the conserved residues of the family of protein serine/threonine kinases indicate that the polypeptides of the invention are serine/threonine kinases. The homology studies described below for each of these six sequences provide additional support for their activity as serine/threonine kinases.

MDCK-1

As noted above, three of the cDNAs (MDCK-1, MDCK-2 and MDCK-3) were isolated from murine (*Mus musculus* C57 Black6) dendritic cells. MDCK-1 (SEQ ID NO:1)

encodes an open reading frame (nucleotides 71-1009) which commences with an ATG coding for a methionine residue and ends with an in-frame stop codon. In addition, the predicted polypeptide of MDCK-1 (SEQ ID NO:8, 275 amino acids) contains a canonical protein serine/threonine kinase domain from amino acid residues 25 to 296.

5 In initial searches of public databases using the BLAST algorithm, it was found that MDCK-1 closely resembles the following GenBank entries: Accession # AF096300, HPK/GCK-like kinase (HGK) [Homo sapiens] (85% amino acid identity, 248 out of 291 amino acid residues); Accession # U88984, Nck-interacting kinase (NIK) [Mus musculus] (83% amino acid identity, 243 out of 291 amino acid residues); Accession # AB011123, KIAA0551 protein [Homo sapiens] (85% amino acid identity, 225 out of 264 amino acid residues). A search of the Derwent GeneSeq patent database using the BLAST algorithm revealed: Human protein kinase SOK-1 (Ste20 oxidant stress response kinase protein) which has 46% amino acid identity with MDCK-1 and Human protein kinase HPK, which has 44% amino acid identity with MDCK-1. In the kinase domain, the strongest homology of MDCK-1 was found to be with human HPK/GCK-like kinase HGK (Accession AF096300, 85% amino acid identity) and murine NIK (Accession U88984, 83% amino acid identity) although there are close similarities with a number of other members of a growing subfamily of kinases collectively termed the GC-kinases (for Germinal Center Kinases).

15 In more recent searches of public databases using BLAST, the following Genbank protein sequences were found to have even greater sequence similarity to the MDCK-1 polypeptide: Accession # AB035697, Misshapen/NIKs-related kinase MINK-1 [Mus musculus] (100% amino acid identity, 275 of 275 residues); Accession # AB041925, GCK family kinase MINK-2 [Mus musculus] (100% amino acid identity, 275 of 275 residues); Accession # AB035698, Misshapen/NIKs-related kinase MINK-1 [Homo sapiens] (99% amino acid identity, 274 of 275 residues); Accession # AB041926, GCK family kinase MINK-2 [Homo sapiens] (99% amino acid identity, 274 of 275 residues). MINK is a novel GCK family kinase that is most abundant in brain. Its expression is up-regulated in the course of the postnatal development of mouse cerebrum. MINK is an upstream activator of the stress-activated protein kinase cascade. MINK-2 is an alternatively spliced form of MINK-1; a splicing cassette consisting of 24 bp encoding a 6 amino acid polypeptide is inserted. MINK-2 is more abundant than MINK-1 in mouse brain. The search of the Derwent GeneSeq patent database using the BLAST algorithm revealed: Accession #

Y55931, Human ZC1 protein (91 % amino acid identity, 251 of 275 residues); Accession # Y55954, Mouse STE20-related protein kinase NIK protein (89 % amino acid identity, 246 of 275 residues); Accession # Y55933, Human ZC3 protein (98 % amino acid identity, 236 of 240 residues); Accession # Y55953, Nematode STE20-related protein kinase ZC504.4 protein (82 % amino acid identity, 221 of 268 residues; and Accession # Y55932, Human ZC2 protein. protein (90 % amino acid identity, 216 of 239 residues).

MDCK-1 is clearly a member of the GCK family which includes the NcK interacting kinase family (NIK). GCK kinases are a subfamily of the Sterile20 (STE-20) protein kinases. This family of kinases are involved as upstream activators of the Jun terminal kinases (JNK's) which are characteristically activated in response to a variety of cellular stresses. The properties of these kinases were recently reviewed [Kyriakis JM, 1999, Signaling by the germinal center kinase family of protein kinases, *J. Biol. Chem.* 274(9): 5259-62; which is incorporated by reference herein]. The sequence of the MDCK-1 polypeptide indicates that it may be a truncated version of murine MINK; however, MDCK-1 protein contains an intact kinase domain and is predicted to form a catalytically functional kinase when expressed in host cells, and therefore can be used to modulate or regulate these pathways in disease conditions, and to identify activators and inhibitors of these pathways.

#### MDCK-2

The MDCK-2 cDNA was isolated from murine dendritic cells. Nucleotides 115-1020 of MDCK-2 (SEQ ID NO:2) encode an open reading frame with three possible in-frame initiator methionines at amino acid residues 1, 8, and 26. All three of these methionine residues are upstream of the first kinase subdomain. Any one or more of them could be the physiologically relevant initiator Met; however, amino acid sequence similarity to human NEK5 protein suggests that the methionine at the first position is the initiator Met residue. SEQ ID NO:9 shows the open reading frame with a predicted polypeptide of 304 amino acids. Like MDCK-1, MDCK-2 contains a canonical protein serine/threonine kinase domain (amino acid residues 34-295 of SEQ ID NO:9).

In initial searches of the public databases using the BLAST algorithm it was found that MDCK-2 most closely resembles a GenBank entry: Accession # Z50873. MDCK-2 demonstrated 77% amino acid amino acid identity (189 out of 245 residues) to this putative kinase from *Caenorhabditis elegans*. MDCK-2 also appeared related to the NEK (NIMA-

related protein kinase) family of kinases. A BLAST search of the Derwent patent database indicated a human kinase called HPK-1 has 85% amino acid amino acid identity with MDCK-2 protein over a 232 amino acid span.

In more recent searches of the public databases using BLAST, the following Genbank  
5 protein sequence was found to have sequence similarity to the MDCK-2 polypeptide:  
Accession # AB026289, protein kinase SID6-1512 [Homo sapiens] (81% amino acid identity,  
238 of 291 residues). The search of the Derwent GeneSeq patent database using the BLAST  
algorithm revealed: Accession # Y59143, Human serine/threonine kinase, NEK5 protein (97  
% amino acid identity, 295 of 302 residues). MDCK-2 appears to be the murine homologue  
10 of human NEK5, and there are several other NEKs that are closely related to MDCK-2. The  
NEKs were named based on their relationship with the NIMA family (NIMA-related kinase),  
which are proteins that regulate mitosis and mitogenesis.

### MDCK-3

15 MDCK-3 was isolated from murine dendritic cells and encodes an open reading  
frame of 355 amino acids (nucleotides 243-1310 of SEQ ID NO:3) which contains a  
canonical serine/threonine kinase domain (amino acid residues 23-279 of SEQ ID NO:10 and  
Figure 3).

Initial searches of available protein sequence databases revealed that MDCK-3 had  
20 not previously been described. The closest homolog in these databases was rat  
calcium/calmodulin - dependent kinase 1 (Genbank accession Q63450) which shares 77.7%  
sequence amino acid identity with MDCK-3.

In more recent searches of the public databases using BLAST, the following Genbank  
protein sequences were found to have sequence similarity to the MDCK-3 polypeptide:  
25 Accession # AAA66944, CaM-like protein kinase [Rattus norvegicus] (84% amino acid  
identity, 266 of 314 residues); Accession # AAA99458, cam kinase I [Homo sapiens] (84%  
amino acid identity, 265 of 314 residues); and Accession # AAA19670, protein kinase I  
[Rattus norvegicus] (83% amino acid identity, 263 of 314 residues). The search of the  
Derwent GeneSeq patent database using the BLAST algorithm revealed additional  
30 calcium/calmodulin-dependent protein kinases as having similarity to MDCK-3, but none  
that shared more than 70% amino acid sequence amino acid identity with MDCK-3. From

these results it is clear that MDCK-3 is a member of the Ca<sup>2+</sup>/calmodulin-dependent kinase family.

MDCK-3 RNA has been found to be expressed in certain cancer cell lines, but not in others (see the table below); thus, MDCK-3 may be useful as a marker for the presence  
5 certain cancer types, such as colon cancer or ovarian cancer.

Cancer Cell Line:	Cancer Type:	MDCK-3 Expression:
Colo205	colon carcinoma	+
HT29	colon carcinoma	+
IGROV-1	ovarian carcinoma	+
MDA231	breast adenocarcinoma	+
Jurkat	T-cell leukemia	-
MALME-3M	melanoma	-
WM9	melanoma	-
WM-35	melanoma	-
WM164	melanoma	-
WM-3211	melanoma	+

MDCK-3 RNA has also been demonstrated to be regulated in response to dendritic cell maturation and/or activation, as described in Example 7.

10

#### MLSK-1

Two additional clones, MLSK-1 and MLSK-2, were isolated from murine lymph node stromal cells. MLSK-1 (SEQ ID NO:11) contains an open reading frame encoded by nucleotides 123-2015 of SEQ ID NO:4, which commences with an ATG coding for a  
15 methionine residue and ends with an in-frame stop codon. The predicted 631 amino acid sequence (SEQ ID NO:11) contains a canonical protein serine/threonine kinase domain at residues 57 to 309.

In initial searches of public databases using the BLAST algorithm it was found that MLSK-1 most closely resembles (61.5% amino acid identity, 281 of 452 residues) a putative  
20 human protein called KIAA0537 (GenBank accession # AB011109), which also appears to encode a protein kinase. MLSK-1 is not likely to simply be the murine homolog of

KIAA0537, however, since there is an example of a publicly-available human EST (AI469033) that shares a higher percentage amino acid identity (87%) with MLSK-1 over 477 predicted residues than does KIAA0537. Generally, MLSK-1 most closely resembles a subset of the protein kinase superfamily known as the adenosine monophosphate (AMP) kinases (AMPK's). More recent database searches have not revealed any sequences more similar to MLSK-1.

As described in Example 8, we have expressed an active form of MLSK-1 and shown that when over-expressed in COS cells it activates the MAP kinase signaling pathway as evidenced by the generation of phosphorylated forms of ERK (Extracellularly Regulated Kinase), and therefore is likely involved in a pathway regulating mitogenesis. Over-expression of MLSK-1 had no effect on the stress-activated kinase pathway, as it did not result in activation of either JNK nor p38 kinases.

As described in Example 9, assays to determine whether MLSK-1 could activate the transcription factor AP-1 were performed. AP-1 is a transcription factor known to be involved in the JNK and p38 signaling pathways. MLSK-1 was co-transfected with an AP-1-luciferase construct into COS-7 cells in a standard AP-1-luciferase reporter assay. The overexpression of MLSK-1 did not activate AP-1 using this assay system.

We obtained some preliminary data on MLSK-1 substrate specificity using a PhosphoSpots™ assay, as described in Example 5. This is a membrane which has coupled to it 20 different peptide sequences that are known to have sites recognized by known kinases. MLSK-1 added phosphate residues to a number of peptide substrates recognized by kinases, and in particular those such as protein kinase C, p34 cdc2 kinase, and one of the p42/p44 MAP kinase substrates.

## 25        MLSK-2

In MLSK-2, nucleotides 121 to 1053 of SEQ ID NO:5 encode an open reading frame which ends with an in-frame stop codon. The predicted polypeptide of 311 amino acids of SEQ ID NO:12 contains a methionine at position 1 from which translation is presumably initiated. The sequence C-terminal to this methionine contains little more than a canonical protein serine/threonine kinase domain. There are currently no close homologs of MLSK-2 in the protein sequence databases. There are two publicly-available human ESTs (GenBank Accession numbers AA018361 and AI333117) that are highly similar to regions of MLSK-2



(88% identical over 156 predicted residues, and 97% identical over 116 residues, respectively), implying a high degree of sequence conservation of this kinase.

In more recent searches of the public databases using BLAST, the following Genbank protein sequence was found to have sequence similarity to the MLSK-2 polypeptide:

5 Accession # AL117482 hypothetical protein [Homo sapiens] (92% amino acid identity, 205 of 221 residues). The search of the Derwent GeneSeq patent database using the BLAST algorithm revealed: Accession # Y27057, Human protein kinase HKPM-6 (97 % amino acid identity, 199 of 205 residues); and Accession # Y23755, Protein involved in eliciting a signal in HH-PTC, human homologue of the *Drosophila fused* gene (95 % amino acid identity, 196  
10 of 206 residues).

As with MLSK-1, we have expressed an active form of MLSK-2 and shown that when over-expressed in COS cells it activates the MAP kinase signaling pathway as evidenced by the generation of phosphorylated forms of ERK. Over-expression of MLSK-2 had no effect on the stress-activated kinase pathway, i.e it did not activate either JNK nor p38  
15 kinases. (See Example 8 below.)

As was done with MLSK-1, assays to determine whether MLSK-2 could activate the transcription factor AP-1 were performed. MLSK-2 was co-transfected with an AP-1-luciferase construct into COS-7 cells in a standard AP-1-luciferase reporter assay. The overexpression of MLSK-2 did not activate AP-1 using this assay system. (See Example 9  
20 below.)

#### ss4694 and LNRK-1

A protein serine/threonine kinase was isolated from human dendritic cells, beginning with a novel protein serine/threonine kinase called ss4694 (SEQ ID NO:6); the nucleotide  
25 sequence of which codes for a methionine followed by an open reading frame of 261 amino acids (SEQ ID NO:13). Included in this open reading frame are conserved motifs found in all protein kinases. The predicted amino acids 27 through 257 of SEQ ID NO:13 are identical to the N-terminal 230 amino acids of an incomplete protein kinase KIAA0551 (GenBank Accession #AB011123). In fact, ss4694 provides the missing 27 amino-acid N-  
30 terminal region of KIAA051. This is significant because this N-terminal sequence cannot be found in any public database at this time. By combining the two sequences ss4694 and KIAA0551, a full-length transcript of 4.08 kb can be predicted as shown in SEQ ID NO:7.

The translation of this sequence, which we call LNRK-1 (Large NIK-Related Kinase-1), is shown as SEQ ID:14.

By using PCR primers based upon the sequence of ss4694, it was determined by performing an RT-PCR assay (as described in Example 7 below) that the kinase was expressed at relatively high levels in human spleen. 5' and 3' flanking PCR primers (5' primer: ATGGCGAGCGACTCCCCGGCTCGAA (SEQ ID NO:15); 3' primer: CCAGTTCATCATGGAATTTCTGTTGAGGG (SEQ ID NO:16)) were then designed based upon the predicted full-length sequence of LNRK-1 and were used to amplify a 4.08 kb cDNA from a Clontech Marathon-ready human spleen cDNA library. Sequencing of this PCR product confirmed its identity with the sequence predicted for LNRK-1.

In initial searches of the public databases, the strongest homology in the kinase domain of LNRK-1 is with murine NIK (GenBank Accession #U88984) and human HPK/GCK-like kinase HGK (GenBank Accession #AF096300). There are also close similarities to a number of other members of a growing family of kinases collectively termed the GC-kinases (Germinal Center Kinases) (Kyrakis, JM, 1999, Signaling by the germinal center kinase family of protein kinases, *J Biol Chem* 274(9): 5259-62). Generally these kinases are implicated as upstream activators of the Jun terminal kinases (JNK's) which are characteristically activated in response to a variety of cellular stresses.

In more recent searches of the public databases using BLAST, the following Genbank protein sequence was found to have sequence similarity to the LNRK-1 polypeptide: Accession # AF172264, Traf2 and NCK interacting kinase, splice variant 1 [Homo sapiens] (100% amino acid identity, 1360 of 1360 residues). The search of the Derwent GeneSeq patent database using the BLAST algorithm revealed: Accession # Y55932, Human ZC2 (92% amino acid identity, 927 of 1002 residues). LNRK-1 is identical to one of the eight splice variants identified for the Traf2 and Nck interacting kinase "TNIK" of GenBank Accession # AF172264. The ZC2 protein of GeneSeq Accession # Y55932 appears to be identical or at least related to another of these "TNIK" splice variants. TNIK is described as a Novel Germinal Center Kinase Family Member That Activates The JNK Pathway and Regulates The Cytoskeleton (Fu *et al.*, 1999, *J. Biol. Chem.* 274 (43): 30729-30737; which is incorporated by reference herein).

We have assayed the tissue-specific expression for LNRK-1 as reported in Example 7, and found roughly equivalent ubiquitous expression of it with slightly higher levels in PBL and slightly lower levels in kidney, skeletal muscle, and small intestine.

5           Fragments

The invention also provides polypeptides and fragments of the kinase domain of polypeptides of the invention that retain a desired biological activity. Particular embodiments are directed to polypeptide fragments that retain the ability to bind a "binding partner" or native cognates, substrates, or counter-structure molecules. Such a fragment may be a  
10 soluble polypeptide. In another embodiment, the polypeptides and fragments advantageously include regions that are conserved in the kinase family.

Also provided herein are polypeptide fragments comprising at least 10, at least 20, or at least 30, contiguous amino acids of the sequence of SEQ ID NOs:8-14. Fragments derived from different domains find use in studies of signal transduction, and in regulating  
15 cellular processes associated with transduction of biological signals. Polypeptide fragments also may be employed as immunogens, in generating antibodies.

Variants

Naturally occurring variants as well as derived variants of the polypeptides and  
20 fragments are provided herein.

Variants may exhibit amino acid sequences that are at least 80% identical. Also contemplated are embodiments in which a polypeptide or fragment comprises an amino acid sequence that is at least 90% identical, at least 95% identical, at least 98% identical, at least 99% identical, or at least 99.9% identical to the preferred polypeptide or fragment thereof.  
25 Percent identity may be determined by visual inspection and mathematical calculation. Alternatively, the percent identity of two protein sequences can be determined by comparing sequence information using the GAP computer program, based on the algorithm of Needleman and Wunsch (J. Mol. Bio. 48:443, 1970) and available from the University of Wisconsin Genetics Computer Group (UWGCG). The preferred default parameters for the  
30 GAP program include: (1) a scoring matrix, blosum62, as described by Henikoff and Henikoff (Proc. Natl. Acad. Sci. USA 89:10915, 1992); (2) a gap weight of 12; (3) a gap

length weight of 4; and (4) no penalty for end gaps. Other programs used by one skilled in the art of sequence comparison may also be used.

The variants of the invention include, for example, those that result from alternate mRNA splicing events or from proteolytic cleavage. Alternate splicing of mRNA may, for example, yield a truncated but biologically active protein, such as a naturally occurring soluble form of the protein. Variations attributable to proteolysis include, for example, differences in the N- or C-termini upon expression in different types of host cells, due to proteolytic removal of one or more terminal amino acids from the protein (generally from 1-5 terminal amino acids). Proteins in which differences in amino acid sequence are attributable to genetic polymorphism (allelic variation among individuals producing the protein) are also contemplated herein.

Additional variants within the scope of the invention include polypeptides that may be modified to create derivatives thereof by forming covalent or aggregative conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like. Covalent derivatives may be prepared by linking the chemical moieties to functional groups on amino acid side chains or at the N-terminus or C-terminus of a polypeptide. Conjugates comprising diagnostic (detectable) or therapeutic agents attached thereto are contemplated herein, as discussed in more detail below.

Other derivatives include covalent or aggregative conjugates of the polypeptides with other proteins or polypeptides, such as by synthesis in recombinant culture as N-terminal or C-terminal fusions. Examples of fusion proteins are discussed below in connection with oligomers. Further, fusion proteins can comprise peptides added to facilitate purification and identification. Such peptides include, for example, poly-His or the antigenic identification peptides described in U.S. Patent No. 5,011,912 and in Hopp et al., *Bio/Technology* 6:1204, 1988. One such peptide is the FLAG<sup>®</sup> peptide, Asp-Tyr-Lys-Asp-Asp-Asp-Asp-Lys, which is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody, enabling rapid assay and facile purification of expressed recombinant protein. A murine hybridoma designated 4E11 produces a monoclonal antibody that binds the FLAG<sup>®</sup> peptide in the presence of certain divalent metal cations, as described in U.S. Patent 5,011,912, hereby incorporated by reference. The 4E11 hybridoma cell line has been deposited with the American Type Culture Collection under accession no. HB 9259.

Monoclonal antibodies that bind the FLAG<sup>®</sup> peptide are available from Eastman Kodak Co., Scientific Imaging Systems Division, New Haven, Connecticut.

Among the variant polypeptides provided herein are variants of native polypeptides that retain the native biological activity or the substantial equivalent thereof. One example  
5 is a variant that binds with essentially the same binding affinity as does the native form. Binding affinity can be measured by conventional procedures, *e.g.*, as described in U.S. Patent No. 5,512,457 and as set forth below.

Variants include polypeptides that are substantially homologous to the native form, but which have an amino acid sequence different from that of the native form because of one  
10 or more deletions, insertions or substitutions. Particular embodiments include, but are not limited to, polypeptides that comprise from one to ten deletions, insertions or substitutions of amino acid residues, when compared to a native sequence.

A given amino acid may be replaced, for example, by a residue having similar physiochemical characteristics. Examples of such conservative substitutions include  
15 substitution of one aliphatic residue for another, such as Ile, Val, Leu, or Ala for one another; substitutions of one polar residue for another, such as between Lys and Arg, Glu and Asp, or Gln and Asn; or substitutions of one aromatic residue for another, such as Phe, Trp, or Tyr for one another. Other conservative substitutions, *e.g.*, involving substitutions of entire regions having similar hydrophobicity characteristics, are well known.

20 Similarly, the DNAs of the invention include variants that differ from a native DNA sequence because of one or more deletions, insertions or substitutions, but that encode a biologically active polypeptide.

The invention further includes polypeptides of the invention with or without associated native-pattern glycosylation. Polypeptides expressed in yeast or mammalian  
25 expression systems (*e.g.*, COS-1 or COS-7 cells) can be similar to or significantly different from a native polypeptide in molecular weight and glycosylation pattern, depending upon the choice of expression system. Expression of polypeptides of the invention in bacterial expression systems, such as *E. coli*, provides non-glycosylated molecules. Further, a given preparation may include multiple differentially glycosylated species of the protein. Glycosyl  
30 groups can be removed through conventional methods, in particular those utilizing glycopeptidase. In general, glycosylated polypeptides of the invention can be incubated with a molar excess of glycopeptidase (Boehringer Mannheim).

Correspondingly, similar DNA constructs that encode various additions or substitutions of amino acid residues or sequences, or deletions of terminal or internal residues or sequences are encompassed by the invention. For example, N-glycosylation sites in the polypeptide extracellular domain can be modified to preclude glycosylation, allowing  
5 expression of a reduced carbohydrate analog in mammalian and yeast expression systems. N-glycosylation sites in eukaryotic polypeptides are characterized by an amino acid triplet Asn-X-Y, wherein X is any amino acid except Pro and Y is Ser or Thr. Appropriate substitutions, additions, or deletions to the nucleotide sequence encoding these triplets will result in prevention of attachment of carbohydrate residues at the Asn side chain. Alteration  
10 of a single nucleotide, chosen so that Asn is replaced by a different amino acid, for example, is sufficient to inactivate an N-glycosylation site. Alternatively, the Ser or Thr can be replaced with another amino acid, such as Ala. Known procedures for inactivating N-glycosylation sites in proteins include those described in U.S. Patent 5,071,972 and EP 276,846, hereby incorporated by reference.

15 In another example of variants, sequences encoding Cys residues that are not essential for biological activity can be altered to cause the Cys residues to be deleted or replaced with other amino acids, preventing formation of incorrect intramolecular disulfide bridges upon folding or renaturation.

Other variants are prepared by modification of adjacent dibasic amino acid residues, to enhance expression in yeast systems in which KEX2 protease activity is present. EP  
20 212,914 discloses the use of site-specific mutagenesis to inactivate KEX2 protease processing sites in a protein. KEX2 protease processing sites are inactivated by deleting, adding or substituting residues to alter Arg-Arg, Arg-Lys, and Lys-Arg pairs to eliminate the occurrence of these adjacent basic residues. Lys-Lys pairings are considerably less susceptible to KEX2  
25 cleavage, and conversion of Arg-Lys or Lys-Arg to Lys-Lys represents a conservative and preferred approach to inactivating KEX2 sites.

#### PRODUCTION OF POLYPEPTIDES AND FRAGMENTS THEREOF

Expression, isolation and purification of the polypeptides and fragments of the  
30 invention may be accomplished by any suitable technique, including but not limited to the following:

### Expression Systems

The present invention provides recombinant cloning and expression vectors containing DNA, as well as host cell containing the recombinant vectors. Expression vectors comprising DNA may be used to prepare the polypeptides or fragments of the invention encoded by the DNA. A method for producing polypeptides comprises culturing host cells transformed with a recombinant expression vector encoding the polypeptide, under conditions that promote expression of the polypeptide, then recovering the expressed polypeptides from the culture. The skilled artisan will recognize that the procedure for purifying the expressed polypeptides will vary according to such factors as the type of host cells employed, and whether the polypeptide is membrane-bound or a soluble form that is secreted from the host cell.

Any suitable expression system may be employed. The vectors include a DNA encoding a polypeptide or fragment of the invention, operably linked to suitable transcriptional or translational regulatory nucleotide sequences, such as those derived from a mammalian, microbial, viral, or insect gene. Examples of regulatory sequences include transcriptional promoters, operators, or enhancers, an mRNA ribosomal binding site, and appropriate sequences which control transcription and translation initiation and termination. Nucleotide sequences are operably linked when the regulatory sequence functionally relates to the DNA sequence. Thus, a promoter nucleotide sequence is operably linked to a DNA sequence if the promoter nucleotide sequence controls the transcription of the DNA sequence. An origin of replication that confers the ability to replicate in the desired host cells, and a selection gene by which transformants are identified, are generally incorporated into the expression vector.

In addition, a sequence encoding an appropriate signal peptide (native or heterologous) can be incorporated into expression vectors. A DNA sequence for a signal peptide (secretory leader) may be fused in frame to the nucleic acid sequence of the invention so that the DNA is initially transcribed, and the mRNA translated, into a fusion protein comprising the signal peptide. A signal peptide that is functional in the intended host cells promotes extracellular secretion of the polypeptide. The signal peptide is cleaved from the polypeptide upon secretion of polypeptide from the cell.

The skilled artisan will also recognize that the position(s) at which the signal peptide is cleaved may differ from that predicted by computer program, and may vary according to

such factors as the type of host cells employed in expressing a recombinant polypeptide. A protein preparation may include a mixture of protein molecules having different N-terminal amino acids, resulting from cleavage of the signal peptide at more than one site.

Suitable host cells for expression of polypeptides include prokaryotes, yeast or higher eukaryotic cells. Mammalian or insect cells are generally preferred for use as host cells. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described, for example, in Pouwels et al. *Cloning Vectors: A Laboratory Manual*, Elsevier, New York, (1985). Cell-free translation systems could also be employed to produce polypeptides using RNAs derived from DNA constructs disclosed herein.

#### Prokaryotic Systems

Prokaryotes include gram-negative or gram-positive organisms. Suitable prokaryotic host cells for transformation include, for example, *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium*, and various other species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*. In a prokaryotic host cell, such as *E. coli*, a polypeptide may include an N-terminal methionine residue to facilitate expression of the recombinant polypeptide in the prokaryotic host cell. The N-terminal Met may be cleaved from the expressed recombinant polypeptide.

Expression vectors for use in prokaryotic host cells generally comprise one or more phenotypic selectable marker genes. A phenotypic selectable marker gene is, for example, a gene encoding a protein that confers antibiotic resistance or that supplies an autotrophic requirement. Examples of useful expression vectors for prokaryotic host cells include those derived from commercially available plasmids such as the cloning vector pBR322 (ATCC 37017). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells. An appropriate promoter and a DNA sequence are inserted into the pBR322 vector. Other commercially available vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotec, Madison, WI, USA).

Promoter sequences commonly used for recombinant prokaryotic host cell expression vectors include  $\beta$ -lactamase (penicillinase), lactose promoter system (Chang et al., *Nature* 275:615, 1978; and Goeddel et al., *Nature* 281:544, 1979), tryptophan (trp) promoter system



(Goeddel et al., *Nucl. Acids Res.* 8:4057, 1980; and EP-A-36776) and tac promoter (Maniatis, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, p. 412, 1982).

A particularly useful prokaryotic host cell expression system employs a phage  $\lambda P_L$  promoter and a cI857ts thermolabile repressor sequence. Plasmid vectors available from the American  
5 Type Culture Collection which incorporate derivatives of the  $\lambda P_L$  promoter include plasmid pHUB2 (resident in *E. coli* strain JMB9, ATCC 37092) and pPLc28 (resident in *E. coli* RR1, ATCC 53082).

### Yeast Systems

10 Alternatively, the polypeptides may be expressed in yeast host cells, preferably from the *Saccharomyces* genus (e.g., *S. cerevisiae*). Other genera of yeast, such as *Pichia* or *Kluyveromyces*, may also be employed. Yeast vectors will often contain an origin of replication sequence from a 2 $\mu$  yeast plasmid, an autonomously replicating sequence (ARS), a promoter region, sequences for polyadenylation, sequences for transcription termination,  
15 and a selectable marker gene. Suitable promoter sequences for yeast vectors include, among others, promoters for metallothionein, 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073, 1980) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149, 1968; and Holland et al., *Biochem.* 17:4900, 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase,  
20 glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phospho-glucose isomerase, and glucokinase. Other suitable vectors and promoters for use in yeast expression are further described in Hitzeman, EPA-73,657. Another alternative is the glucose-repressible ADH2 promoter described by Russell et al. (*J. Biol. Chem.* 258:2674, 1982) and Beier et al. (*Nature* 300:724, 1982). Shuttle vectors  
25 replicable in both yeast and *E. coli* may be constructed by inserting DNA sequences from pBR322 for selection and replication in *E. coli* (Amp<sup>r</sup> gene and origin of replication) into the above-described yeast vectors.

The yeast  $\alpha$ -factor leader sequence may be employed to direct secretion of the polypeptide. The  $\alpha$ -factor leader sequence is often inserted between the promoter sequence  
30 and the structural gene sequence. See, e.g., Kurjan et al., *Cell* 30:933, 1982 and Bitter et al., *Proc. Natl. Acad. Sci. USA* 81:5330, 1984. Other leader sequences suitable for facilitating secretion of recombinant polypeptides from yeast hosts are known to those of skill in the art.

A leader sequence may be modified near its 3' end to contain one or more restriction sites. This will facilitate fusion of the leader sequence to the structural gene.

Yeast transformation protocols are known to those of skill in the art. One such protocol is described by Hinnen et al., *Proc. Natl. Acad. Sci. USA* 75:1929, 1978. The  
5 Hinnen et al. protocol selects for Trp<sup>+</sup> transformants in a selective medium, wherein the selective medium consists of 0.67% yeast nitrogen base, 0.5% casamino acids, 2% glucose, 10 mg/ml adenine and 20 mg/ml uracil.

Yeast host cells transformed by vectors containing an ADH2 promoter sequence may be grown for inducing expression in a "rich" medium. An example of a rich medium is one  
10 consisting of 1% yeast extract, 2% peptone, and 1% glucose supplemented with 80 mg/ml adenine and 80 mg/ml uracil. Derepression of the ADH2 promoter occurs when glucose is exhausted from the medium.

#### Mammalian or Insect Systems

15 Mammalian or insect host cell culture systems also may be employed to express recombinant polypeptides. Bacculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, *Bio/Technology* 6:47 (1988). Established cell lines of mammalian origin also may be employed. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman et al.,  
20 *Cell* 23:175, 1981), L cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, HeLa cells, and BHK (ATCC CRL 10) cell lines, and the CV1/EBNA cell line derived from the African green monkey kidney cell line CV1 (ATCC CCL 70) as described by McMahan et al. (*EMBO J.* 10: 2821, 1991).

Established methods for introducing DNA into mammalian cells have been described  
25 (Kaufman, R.J., *Large Scale Mammalian Cell Culture*, 1990, pp. 15-69). Additional protocols using commercially available reagents, such as Lipofectamine lipid reagent (Gibco/BRL) or Lipofectamine-Plus lipid reagent, can be used to transfect cells (Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413-7417, 1987). In addition, electroporation can be used to transfect mammalian cells using conventional procedures, such as those in Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, 2 ed. Vol. 1-3, Cold Spring Harbor  
30 Laboratory Press, 1989). Selection of stable transformants can be performed using methods known in the art, such as, for example, resistance to cytotoxic drugs. Kaufman et al., *Meth.*

in *Enzymology* 185:487-511, 1990, describes several selection schemes, such as dihydrofolate reductase (DHFR) resistance. A suitable host strain for DHFR selection can be CHO strain DX-B11, which is deficient in DHFR (Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA* 77:4216-4220, 1980). A plasmid expressing the DHFR cDNA can be introduced into strain  
5 DX-B11, and only cells that contain the plasmid can grow in the appropriate selective media. Other examples of selectable markers that can be incorporated into an expression vector include cDNAs conferring resistance to antibiotics, such as G418 and hygromycin B. Cells harboring the vector can be selected on the basis of resistance to these compounds.

Transcriptional and translational control sequences for mammalian host cell  
10 expression vectors can be excised from viral genomes. Commonly used promoter sequences and enhancer sequences are derived from polyoma virus, adenovirus 2, simian virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early and late promoter, enhancer, splice, and polyadenylation sites can be used to provide other genetic elements for expression of a structural gene sequence  
15 in a mammalian host cell. Viral early and late promoters are particularly useful because both are easily obtained from a viral genome as a fragment, which can also contain a viral origin of replication (Fiers et al., *Nature* 273:113, 1978; Kaufman, *Meth. in Enzymology*, 1990). Smaller or larger SV40 fragments can also be used, provided the approximately 250 bp sequence extending from the *Hind* III site toward the *Bgl* I site located in the SV40 viral  
20 origin of replication site is included.

Additional control sequences shown to improve expression of heterologous genes from mammalian expression vectors include such elements as the expression augmenting sequence element (EASE) derived from CHO cells (Morris et al., *Animal Cell Technology*, 1997, pp. 529-534 and PCT Application WO 97/25420) and the tripartite leader (TPL) and  
25 VA gene RNAs from Adenovirus 2 (Gingeras et al., *J. Biol. Chem.* 257:13475-13491, 1982). The internal ribosome entry site (IRES) sequences of viral origin allows dicistronic mRNAs to be translated efficiently (Oh and Sarnow, *Current Opinion in Genetics and Development* 3:295-300, 1993; Ramesh et al., *Nucleic Acids Research* 24:2697-2700, 1996). Expression of a heterologous cDNA as part of a dicistronic mRNA followed by the gene for a selectable  
30 marker (e.g. DHFR) has been shown to improve transfectability of the host and expression of the heterologous cDNA (Kaufman, *Meth. in Enzymology*, 1990). Exemplary expression vectors that employ dicistronic mRNAs are pTR-DC/GFP described by Mosser et al.,

*Biotechniques* 22:150-161, 1997, and p2A5I described by Morris et al., *Animal Cell Technology*, 1997, pp. 529-534.

A useful high expression vector, pCAVNOT, has been described by Mosley et al., *Cell* 59:335-348, 1989. Other expression vectors for use in mammalian host cells can be constructed as disclosed by Okayama and Berg (*Mol. Cell. Biol.* 3:280, 1983). A useful system for stable high level expression of mammalian cDNAs in C127 murine mammary epithelial cells can be constructed substantially as described by Cosman et al. (*Mol. Immunol.* 23:935, 1986). A useful high expression vector, PMLSV N1/N4, described by Cosman et al., *Nature* 312:768, 1984, has been deposited as ATCC 39890. Additional useful mammalian expression vectors are described in EP-A-0367566, and in WO 91/18982, incorporated by reference herein. In yet another alternative, the vectors can be derived from retroviruses.

Additional useful expression vectors, pFLAG<sup>®</sup> and pDC311, can also be used. FLAG<sup>®</sup> technology is centered on the fusion of a low molecular weight (1kD), hydrophilic, FLAG<sup>®</sup> marker peptide to the N-terminus of a recombinant protein expressed by pFLAG<sup>®</sup> expression vectors. pDC311 is another specialized vector used for expressing proteins in CHO cells. pDC311 is characterized by a bicistronic sequence containing the gene of interest and a dihydrofolate reductase (DHFR) gene with an internal ribosome binding site for DHFR translation, an expression augmenting sequence element (EASE), the human CMV promoter, a tripartite leader sequence, and a polyadenylation site.

Regarding signal peptides that may be employed, the native signal peptide may be replaced by a heterologous signal peptide or leader sequence, if desired. The choice of signal peptide or leader may depend on factors such as the type of host cells in which the recombinant polypeptide is to be produced. To illustrate, examples of heterologous signal peptides that are functional in mammalian host cells include the signal sequence for interleukin-7 (IL-7) described in United States Patent 4,965,195; the signal sequence for interleukin-2 receptor described in Cosman et al., *Nature* 312:768 (1984); the interleukin-4 receptor signal peptide described in EP 367,566; the type I interleukin-1 receptor signal peptide described in U.S. Patent 4,968,607; and the type II interleukin-1 receptor signal peptide described in EP 460,846.

### Purification

The invention also includes methods of isolating and purifying the polypeptides and fragments thereof.

### 5      Isolation and Purification

The "isolated" polypeptides or fragments thereof encompassed by this invention are polypeptides or fragments that are not in an environment identical to an environment in which it or they can be found in nature. The "purified" polypeptides or fragments thereof encompassed by this invention are essentially free of association with other proteins or  
10 polypeptides, for example, as a purification product of recombinant expression systems such as those described above or as a purified product from a non-recombinant source such as naturally occurring cells and/or tissues.

In one preferred embodiment, the purification of recombinant polypeptides or fragments can be accomplished using fusions of polypeptides or fragments of the invention  
15 to another polypeptide to aid in the purification of polypeptides or fragments of the invention. Such fusion partners can include the poly-His or other antigenic identification peptides described above as well as the Fc moieties described previously.

With respect to any type of host cell, as is known to the skilled artisan, procedures for purifying a recombinant polypeptide or fragment will vary according to such factors as the  
20 type of host cells employed and whether or not the recombinant polypeptide or fragment is secreted into the culture medium.

In general, the recombinant polypeptide or fragment can be isolated from the host cells if not secreted, or from the medium or supernatant if soluble and secreted, followed by one or more concentration, salting-out, ion exchange, hydrophobic interaction, affinity  
25 purification or size exclusion chromatography steps. As to specific ways to accomplish these steps, the culture medium first can be concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. Following the concentration step, the concentrate can be applied to a purification matrix such as a gel filtration medium. Alternatively, an anion exchange resin can be employed, for  
30 example, a matrix or substrate having pendant diethylaminoethyl (DEAE) groups. The matrices can be acrylamide, agarose, dextran, cellulose or other types commonly employed in protein purification. Alternatively, a cation exchange step can be employed. Suitable

cation exchangers include various insoluble matrices comprising sulfopropyl or carboxymethyl groups. In addition, a chromatofocusing step can be employed. Alternatively, a hydrophobic interaction chromatography step can be employed. Suitable matrices can be phenyl or octyl moieties bound to resins. In addition, affinity chromatography with a matrix  
5 which selectively binds the recombinant protein can be employed. Examples of such resins employed are lectin columns, dye columns, and metal-chelating columns. Finally, one or more reversed-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, (e.g., silica gel or polymer resin having pendant methyl, octyl, octyldecyl or other aliphatic groups) can be employed to further purify the polypeptides.  
10 Some or all of the foregoing purification steps, in various combinations, are well known and can be employed to provide an isolated and purified recombinant protein.

It is also possible to utilize an affinity column comprising a polypeptide-binding protein of the invention, such as a monoclonal antibody generated against polypeptides of the invention, to affinity-purify expressed polypeptides. These polypeptides can be removed  
15 from an affinity column using conventional techniques, e.g., in a high salt elution buffer and then dialyzed into a lower salt buffer for use or by changing pH or other components depending on the affinity matrix utilized, or be competitively removed using the naturally occurring substrate of the affinity moiety, such as a polypeptide derived from the invention.

In this aspect of the invention, polypeptide-binding proteins, such as the anti-  
20 polypeptide antibodies of the invention or other proteins that may interact with the polypeptide of the invention, can be bound to a solid phase support such as a column chromatography matrix or a similar substrate suitable for identifying, separating, or purifying cells that express polypeptides of the invention on their surface. Adherence of polypeptide-binding proteins of the invention to a solid phase contacting surface can be accomplished by  
25 any means, for example, magnetic microspheres can be coated with these polypeptide-binding proteins and held in the incubation vessel through a magnetic field. Suspensions of cell mixtures are contacted with the solid phase that has such polypeptide-binding proteins thereon. Cells having polypeptides of the invention on their surface bind to the fixed polypeptide-binding protein and unbound cells then are washed away. This affinity-binding  
30 method is useful for purifying, screening, or separating such polypeptide-expressing cells from solution. Methods of releasing positively selected cells from the solid phase are known in the art and encompass, for example, the use of enzymes. Such enzymes are preferably

non-toxic and non-injurious to the cells and are preferably directed to cleaving the cell-surface binding partner.

Alternatively, mixtures of cells suspected of containing polypeptide-expressing cells of the invention first can be incubated with a biotinylated polypeptide-binding protein of the invention. Incubation periods are typically at least one hour in duration to ensure sufficient binding to polypeptides of the invention. The resulting mixture then is passed through a column packed with avidin-coated beads, whereby the high affinity of biotin for avidin provides the binding of the polypeptide-binding cells to the beads. Use of avidin-coated beads is known in the art. See Berenson, et al. *J. Cell. Biochem.*, 10D:239 (1986). Wash of unbound material and the release of the bound cells is performed using conventional methods.

The desired degree of purity depends on the intended use of the protein. A relatively high degree of purity is desired when the polypeptide is to be administered *in vivo*, for example. In such a case, the polypeptides are purified such that no protein bands corresponding to other proteins are detectable upon analysis by SDS-polyacrylamide gel electrophoresis (SDS-PAGE). It will be recognized by one skilled in the pertinent field that multiple bands corresponding to the polypeptide may be visualized by SDS-PAGE, due to differential glycosylation, differential post-translational processing, and the like. Most preferably, the polypeptide of the invention is purified to substantial homogeneity, as indicated by a single protein band upon analysis by SDS-PAGE. The protein band may be visualized by silver staining, Coomassie blue staining, or (if the protein is radiolabeled) by autoradiography.

#### USE OF NUCLEIC ACID OR OLIGONUCLEOTIDES OF THE INVENTION

In addition to being used to express polypeptides as described above, the nucleic acids of the invention, including DNA, RNA, mRNA and oligonucleotides thereof can be used as probes to study signal transduction and to identify nucleic acid encoding proteins having kinase activity; as diagnostic disease markers; and as single-stranded sense or antisense oligonucleotides to inhibit expression of polypeptide encoded by the genes of the invention.

### Probes

Among the uses of nucleic acids of the invention is the use of fragments as probes or primers. Such fragments generally comprise at least about 17 contiguous nucleotides of a DNA sequence. In other embodiments, a DNA fragment comprises at least 30, or at least 60, contiguous nucleotides of a DNA sequence.

Because homologs of SEQ ID NOs:1-7 from other mammalian species are contemplated herein, probes based on the DNA sequence of SEQ ID NOs:1-7 may be used to screen cDNA libraries derived from other mammalian species, using conventional cross-species hybridization techniques.

Using knowledge of the genetic code in combination with the amino acid sequences set forth above, sets of degenerate oligonucleotides can be prepared. Such oligonucleotides are useful as primers, e.g., in polymerase chain reactions (PCR), whereby DNA fragments are isolated and amplified.

### Chromosome Mapping

All or a portion of the nucleic acids of SEQ ID NO:1-7, including oligonucleotides, can be used by those skilled in the art using well-known techniques to identify the human chromosome, and the specific locus thereof. Useful techniques include, but are not limited to, using the sequence or portions, including oligonucleotides, as a probe in various well-known techniques such as radiation hybrid mapping (high resolution), in situ hybridization to chromosome spreads (moderate resolution), and Southern blot hybridization to hybrid cell lines containing individual human chromosomes (low resolution).

For example, chromosomes can be mapped by radiation hybridization. First, PCR is performed using the Whitehead Institute/MIT Center for Genome Research Genebridge4 panel of 93 radiation hybrids ([http://www-genome.wi.mit.edu/ftp/distribution/human\\_STS\\_releases/july97/rhmap/genebridge4.html](http://www-genome.wi.mit.edu/ftp/distribution/human_STS_releases/july97/rhmap/genebridge4.html)). Primers are used which lie within a putative exon of the gene of interest and which amplify a product from human genomic DNA, but do not amplify hamster genomic DNA. The results of the PCRs are converted into a data vector that is submitted to the Whitehead/MIT Radiation Mapping site on the internet (<http://www-seq.wi.mit.edu>). The data is scored and the chromosomal assignment and placement relative to known Sequence Tag Site (STS) markers on the radiation hybrid map



is provided. The following web site provides additional information about radiation hybrid mapping: [http://www-genome.wi.mit.edu/ftp/distribution/human\\_STS\\_releases/july97/07-97.INTRO.html](http://www-genome.wi.mit.edu/ftp/distribution/human_STS_releases/july97/07-97.INTRO.html)).

5           Sense-Antisense

Other useful fragments of the nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of DNA  
10 (SEQ ID NOs:1-7). Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to about 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (*Cancer Res.* 48:2659, 1988) and van der Krol et al. (*BioTechniques* 6:958, 1988).

15           Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block or inhibit protein expression by one of several means, including enhanced degradation of the mRNA by RNaseH, inhibition of splicing, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of proteins. Antisense or sense oligonucleotides further  
20 comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

25           Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10448, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides  
30 to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, lipofection, CaPO<sub>4</sub>-mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus.

5        Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not  
10       substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

          Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex,  
15       as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

#### USE OF KINASE POLYPEPTIDES AND FRAGMENTED POLYPEPTIDES

Uses include, but are not limited to, the following:

- 20       - Identifying molecules that modulate kinase activity and cellular responses
- Purifying proteins and measuring activity thereof
- Research Reagents
- Molecular weight and Isoelectric focusing markers
- Controls for peptide fragmentation
- 25       - Identification of unknown proteins
- Preparation of Antibodies
- Therapeutic Compounds

#### Identifying molecules that modulate kinase activity and cellular responses

30       Cellular signaling often involves a molecular activation cascade, during which a receptor propagates a ligand-receptor mediated signal by specifically activating intracellular kinases which phosphorylate target substrates. These substrates can themselves be kinases

which become activated following phosphorylation. Alternatively, they can be adaptor molecules that facilitate down stream signaling through protein-protein interaction following phosphorylation. Regardless of the nature of the substrate molecule(s), expressed functionally active versions of the polypeptides of the invention, for example the kinase domain, can be used in assays to identify molecules that modulate the recognition and activation of substrate(s) by the kinases. These assays include, without limitation, the yeast 1,- 2-, or 3-hybrid assays, or an assay of binding that measures changes in the surface plasmon resonance of a bound molecule (using for example an instrument from BIAcore), or other assays designed for high-throughput screening. Other assays that may be used to identify activators and inhibitors of the kinases of the invention are described without limitation in the Examples below. In this way, these novel kinases can be used in assay methods to identify novel molecules that can modulate the activity of signal transduction pathways and affect the cellular response to external and internal signals.

The purpose of such an assay is to identify substances which modulate substrate phosphorylation. Such inhibitory or activating substances could serve as lead compounds in the development of pharmaceuticals for the treatment of , for example, autoimmune disease, rheumatoid and other inflammatory conditions, cancer, viral infections, asthma, transplant rejection, infectious or neoplastic diseases in which there is a dysregulation of processes mediated by the kinase. It is conceivable that compounds which activate or inhibit the kinases of the invention could have merit as more general modulators of the class of protein kinases which mediate signaling, including (but not limited to) those mentioned herein. Examples of compounds that may modulate kinase activity include but are not limited to catalytically inactive, truncated, or otherwise mutated form of a kinase, preferably a kinase of the present invention; and numerous chemical classes, particularly organic compounds; preferably small organic compounds and are obtained from a wide variety of sources including libraries of synthetic or natural compounds. Preferred modulators of kinase activity are orally active in mammalian hosts. For diagnostic uses, the kinase modulators or other binding agents are frequently labeled, such as with fluorescent, radioactive, chemiluminescent, or other easily detectable molecules, either conjugated directly to the binding agent or conjugated to a probe specific for the binding agent.

### Purification Reagents

Each of the polypeptides of the invention finds use as a protein purification reagent. For example, the polypeptides may be used to purify binding partner proteins. In particular  
5       embodiments, a polypeptide (in any form described herein that is capable of binding a binding partner) is attached to a solid support by conventional procedures. As one example, affinity chromatography columns containing functional groups that will react with functional groups on amino acid side chains of proteins are available (Pharmacia Biotech, Inc., Piscataway, NJ).

10       The polypeptide also finds use in identifying cells that express binding partner proteins. Polypeptides are bound to a solid phase such as a column chromatography matrix or a similar suitable substrate. For example, magnetic microspheres can be coated with the polypeptides and held in an incubation vessel through a magnetic field. Suspensions of cell lysates containing expressed binding partner protein are contacted with the solid phase having  
15       the polypeptides thereon. Binding partner proteins from cells expressing the binding partner bind to the fixed polypeptides, and unbound protein is washed away.

Alternatively, the polypeptides can be conjugated to a detectable moiety, then incubated with cell lysates to be tested for binding partner expression. After incubation, unbound labeled matter is removed and the presence or absence of the detectable moiety is  
20       determined.

In a further alternative, mixtures of cell lysates suspected of containing binding partner protein are incubated with biotinylated polypeptides of the invention. Incubation periods are typically at least one hour in duration to ensure sufficient binding. The resulting mixture then is passed through a column packed with avidin-coated beads, whereby the high  
25       affinity of biotin for avidin provides binding of the desired cells to the beads. Procedures for using avidin-coated beads are known (see Berenson, et al. *J. Cell. Biochem.*, 10D:239, 1986). Washing to remove unbound material, and the release of the bound cells, are performed using conventional methods.

### Measuring Activity

30       Polypeptides also find use in measuring the biological activity of binding partner protein in terms of their binding affinity. The polypeptides thus may be employed by those

conducting "quality assurance" studies, e.g., to monitor shelf life and stability of protein under different conditions. For example, the polypeptides may be employed in a binding affinity study to measure the biological activity of a binding partner protein that has been stored at different temperatures, or produced in different cell types. The proteins also may be used to determine whether biological activity is retained after modification of a binding partner protein (e.g., chemical modification, truncation, mutation, etc.). The binding affinity of the modified binding partner protein is compared to that of an unmodified binding partner protein to detect any adverse impact of the modifications on biological activity of binding partner. The biological activity of a binding partner protein thus can be ascertained before it is used in a research study, for example.

In particularly preferred embodiments, the isolated kinase polypeptide fragments can be used to assay protein kinase activity.

#### Research Agents

Another embodiment of the invention is the use of isolated kinase polypeptides of the invention, fusion proteins, or a fragment thereof containing the isolated protein kinase domain in *in vitro* or *in vivo* assays to determine protein kinase activity. A hallmark of protein kinases is their ability to phosphorylate other proteins and to auto-phosphorylate. Therefore, in one aspect of the invention, the isolated polypeptides with kinase activity can be used in assays to phosphorylate target proteins, radiolabel target proteins with  $^{32}\text{P}$ , and identify proteins having phosphatase activity. Exemplary methods of phosphorylation assays set forth above are disclosed in U.S. Patents 5,447,860 which is incorporated herein by reference. In addition to full length polypeptides, the invention also includes the isolated active kinase domains of kinases which can function as reagents in kinase assays.

Kinase assays are typically carried out by combining a kinase of the invention, or an active kinase domain, with radiolabeled ATP ( $\gamma^{32}\text{P}$ -ATP) and a peptide or protein substrate in a buffer solution. The peptide substrates generally range from 8 to 30 amino acids in length or the substrate may also be a protein known to be phosphorylated readily by a kinase of the invention. Many such general kinase substrates are known, e.g.  $\alpha$  or  $\beta$  casein, histone H1, myelin basic protein, etc. After incubation of this reaction mixture at 20-37°C for a suitable time, the kinase mediated transfer of radioactive phosphate from ATP to the substrate protein or substrate peptide can be determined by methods well known in the art,

such as, for example, spotting the radioactive products onto phosphocellulose paper, followed by washing and liquid scintillation counting, gel electrophoresis followed by autoradiography, and scintillation proximity assay.

Another embodiment of the invention relates to the study of cell signal transduction.

5 The kinases of the invention, like other kinases, could play a central role in immune responses or other cellular process which include cellular signal transduction. As such, alterations in the expression and/or activation of the kinases can have profound effects on a plethora of cellular processes. Expression of cloned kinases, functionally inactive mutants thereof, or the kinase domain can be used to identify the role a particular protein plays in  
10 mediating specific signaling events.

Cellular signaling often involves a molecular activation cascade, during which a receptor propagates a ligand-receptor mediated signal by specifically activating intracellular kinases which phosphorylate target substrates. These substrates can themselves be kinases which become activated following phosphorylation. Alternatively, they can be adaptor  
15 molecules that facilitate down stream signaling through protein-protein interaction following phosphorylation. Regardless of the nature of the substrate molecule(s), expressed functionally active versions of the polypeptides of the invention, for example the kinase domain, can be used in assays such as the yeast 2-hybrid assay to identify what substrate(s) were recognized and activated by the kinase binding partner(s). As such, these novel kinases  
20 can be used as reagents to identify novel molecules involved in signal transduction pathways.

More specifically, MDCK-1 and LNRK-1, with their strong homologies to human HPK/GCK-like kinase HGK and murine NIK and similarities to other members of the GC (for Germinal Center) kinase family, may be implicated as upstream activators of the Jun terminal kinases. Because JNKs are characteristically activated in response to a variety of  
25 cellular signals, MDCK-1 and LNRK-1 (as cDNA, polypeptides, or antibodies) may be used for the study of signal transduction cascades in tissues where the kinases are expressed.

#### Molecular Weight, Isoelectric Point Markers

The polypeptides of the present invention can be subjected to fragmentation into  
30 smaller peptides by chemical and enzymatic means, and the peptide fragments so produced can be used in the analysis of other proteins or polypeptides. For example, such peptide fragments can be used as peptide molecular weight markers, peptide isoelectric point

markers, or in the analysis of the degree of peptide fragmentation. Thus, the invention also includes these polypeptides and peptide fragments, as well as kits to aid in the determination of the apparent molecular weight and isoelectric point of an unknown protein and kits to assess the degree of fragmentation of an unknown protein.

5           Although all methods of fragmentation are encompassed by the invention, chemical fragmentation is a preferred embodiment, and includes the use of cyanogen bromide to cleave under neutral or acidic conditions such that specific cleavage occurs at methionine residues (E. Gross, *Methods in Enz.* 11:238-255, 1967). This can further include additional steps, such as a carboxymethylation step to convert cysteine residues to an unreactive species.

10           Enzymatic fragmentation is another preferred embodiment, and includes the use of a protease such as Asparaginylendo-peptidase, Arginylendo-peptidase, *Achromobacter* protease I, Trypsin, *Staphylococcus aureus* V8 protease, Endoproteinase Asp-N, or Endoproteinase Lys-C under conventional conditions to result in cleavage at specific amino acid residues. Asparaginylendo-peptidase can cleave specifically on the carboxyl side of the  
15           asparagine residues present within the polypeptides of the invention. Arginylendo-peptidase can cleave specifically on the carboxyl side of the arginine residues present within these polypeptides. *Achromobacter* protease I can cleave specifically on the carboxyl side of the lysine residues present within the polypeptides (Sakiyama and Nakat, U.S. Patent No. 5,248,599; T. Masaki et al., *Biochim. Biophys. Acta* 660:44-50, 1981; T. Masaki et al.,  
20           *Biochim. Biophys. Acta* 660:51-55, 1981). Trypsin can cleave specifically on the carboxyl side of the arginine and lysine residues present within polypeptides of the invention. Enzymatic fragmentation may also occur with a protease that cleaves at multiple amino acid residues. For example, *Staphylococcus aureus* V8 protease can cleave specifically on the carboxyl side of the aspartic and glutamic acid residues present within polypeptides (D. W.  
25           Cleveland, *J. Biol. Chem.* 3:1102-1106, 1977). Endoproteinase Asp-N can cleave specifically on the amino side of the asparagine residues present within polypeptides. Endoproteinase Lys-C can cleave specifically on the carboxyl side of the lysine residues present within polypeptides of the invention. Other enzymatic and chemical treatments can likewise be used to specifically fragment these polypeptides into a unique set of specific  
30           peptides.

          Of course, the peptides and fragments of the polypeptides of the invention can also be produced by conventional recombinant processes and synthetic processes well known in

the art. With regard to recombinant processes, the polypeptides and peptide fragments encompassed by invention can have variable molecular weights, depending upon the host cell in which they are expressed.

5 The molecular weight of these polypeptides can also be varied by fusing additional peptide sequences to both the amino and carboxyl terminal ends of polypeptides of the invention. Fusions of additional peptide sequences at the amino and carboxyl terminal ends of polypeptides of the invention can be used to enhance expression of these polypeptides or aid in the purification of the protein. In addition, fusions of additional peptide sequences at the amino and carboxyl terminal ends of polypeptides of the invention will alter some, but  
10 usually not all, of the fragmented peptides of the polypeptides generated by enzymatic or chemical treatment. Of course, mutations can be introduced into polypeptides of the invention using routine and known techniques of molecular biology. For example, a mutation can be designed so as to eliminate a site of proteolytic cleavage by a specific enzyme or a site of cleavage by a specific chemically induced fragmentation procedure. The  
15 elimination of the site will alter the peptide fingerprint of polypeptides of the invention upon fragmentation with the specific enzyme or chemical procedure.

Because the unique amino acid sequence of each fragment specifies a molecular weight, these fragments can thereafter serve as molecular weight markers using such analysis techniques to assist in the determination of the molecular weight of an unknown protein,  
20 polypeptides or fragments thereof. The molecular weight markers of the invention serve particularly well as molecular weight markers for the estimation of the apparent molecular weight of proteins that have similar apparent molecular weights and, consequently, allow increased accuracy in the determination of apparent molecular weight of proteins.

When the invention relates to the use of fragmented peptide molecular weight  
25 markers, those markers are preferably at least 10 amino acids in size. More preferably, these fragmented peptide molecular weight markers are between 10 and 100 amino acids in size. Even more preferable are fragmented peptide molecular weight markers between 10 and 50 amino acids in size and especially between 10 and 35 amino acids in size. Most preferable are fragmented peptide molecular weight markers between 10 and 20 amino acids in size.

30 Among the methods for determining molecular weight are sedimentation, gel electrophoresis, chromatography, and mass spectrometry. A particularly preferred embodiment is denaturing polyacrylamide gel electrophoresis (U. K. Laemmli, *Nature*



227:680-685, 1970). Conventionally, the method uses two separate lanes of a gel containing sodium dodecyl sulfate and a concentration of acrylamide between 6-20%. The ability to simultaneously resolve the marker and the sample under identical conditions allows for increased accuracy. It is understood, of course, that many different techniques can be used for the determination of the molecular weight of an unknown protein using polypeptides of the invention, and that this embodiment in no way limits the scope of the invention.

Each unglycosylated polypeptide or fragment thereof has a pI that is intrinsically determined by its unique amino acid sequence (which pI can be estimated by the skilled artisan using any of the computer programs designed to predict pI values currently available, calculated using any well-known amino acid pKa table, or measured empirically). Therefore these polypeptides and fragments thereof can serve as specific markers to assist in the determination of the isoelectric point of an unknown protein, polypeptide, or fragmented peptide using techniques such as isoelectric focusing. These polypeptide or fragmented peptide markers serve particularly well for the estimation of apparent isoelectric points of unknown proteins that have apparent isoelectric points close to that of the polypeptide or fragmented peptide markers of the invention.

The technique of isoelectric focusing can be further combined with other techniques such as gel electrophoresis to simultaneously separate a protein on the basis of molecular weight and charge. The ability to simultaneously resolve these polypeptide or fragmented peptide markers and the unknown protein under identical conditions allows for increased accuracy in the determination of the apparent isoelectric point of the unknown protein. This is of particular interest in techniques, such as two dimensional electrophoresis (T.D. Brock and M.T. Madigan, *Biology of Microorganisms* 76-77 (Prentice Hall, 6d ed. 1991)), where the nature of the procedure dictates that any markers should be resolved simultaneously with the unknown protein. In addition, with such methods, these polypeptides and fragmented peptides thereof can assist in the determination of both the isoelectric point and molecular weight of an unknown protein or fragmented peptide.

Polypeptides and fragmented peptides can be visualized using two different methods that allow a discrimination between the unknown protein and the molecular weight markers. In one embodiment, the polypeptide and fragmented peptide molecular weight markers of the invention can be visualized using antibodies generated against these markers and conventional immunoblotting techniques. This detection is performed under conventional

conditions that do not result in the detection of the unknown protein. It is understood that it may not be possible to generate antibodies against all polypeptide fragments of the invention, since small peptides may not contain immunogenic epitopes. It is further understood that not all antibodies will work in this assay; however, those antibodies which are able to bind polypeptides and fragments of the invention can be readily determined using conventional techniques.

The unknown protein is also visualized by using a conventional staining procedure. The molar excess of unknown protein to polypeptide or fragmented peptide molecular weight markers of the invention is such that the conventional staining procedure predominantly detects the unknown protein. The level of these polypeptide or fragmented peptide molecular weight markers is such as to allow little or no detection of these markers by the conventional staining method. The preferred molar excess of unknown protein to polypeptide molecular weight markers of the invention is between 2 and 100,000 fold. More preferably, the preferred molar excess of unknown protein to these polypeptide molecular weight markers is between 10 and 10,000 fold and especially between 100 and 1,000 fold.

It is understood of course that many techniques can be used for the determination and detection of molecular weight and isoelectric point of an unknown protein, polypeptides, and fragmented peptides thereof using these polypeptide molecular weight markers and peptide fragments thereof and that these embodiments in no way limit the scope of the invention.

In another embodiment, the analysis of the progressive fragmentation of the polypeptides of the invention into specific peptides (D. W. Cleveland et al., *J. Biol. Chem.* 252:1102-1106, 1977), such as by altering the time or temperature of the fragmentation reaction, can be used as a control for the extent of cleavage of an unknown protein. For example, cleavage of the same amount of polypeptide and unknown protein under identical conditions can allow for a direct comparison of the extent of fragmentation. Conditions that result in the complete fragmentation of the polypeptide can also result in complete fragmentation of the unknown protein.

As to the specific use of the polypeptides and fragmented peptides of the invention as molecular weight markers, the fragmentation of the polypeptide of SEQ ID NOs:8-14 with cyanogen bromide generates a unique set of fragmented peptide molecular weight markers (See Tables I-VI). The distribution of methionine residues determines the number of amino

acids in each peptide and the unique amino acid composition of each peptide determines its molecular weight.

**Table I-Cleavage of MDCK-1 with cyanogen bromide**

Position	From-To	Molecular Weight
1	1 - 1	149.2
8	237 - 239	383.5
7	227 - 236	1003.1
3	57 - 72	1951.0
6	196 - 226	3459.7
4	73 - 105	3892.5
2	2 - 56	5810.6
9	240 - 313	8251.6
5	106 - 195	10037.5

5

**Table II-Cleavage of MDCK-2 with cyanogen bromide**

Position	From-To	Molecular Weight
1	1 - 1	149.2
12	296 - 303	671.7
7	153 - 158	784.9
2	2 - 8	793.8
10	230 - 241	1327.5
3	9 - 26	2038.4
9	204 - 229	3102.5
6	123 - 152	3744.5
8	159 - 203	4838.6
4	27 - 71	5089.9
5	72 - 122	5790.5
11	242 - 295	6385.2

**Table III-Cleavage of MDCK-3 with cyanogen bromide**

Position	From-To	Molecular Weight
1	1 - 1	149.2
6	172 - 178	734.8
5	163 - 171	997.2

4	139 - 162	2878.2
9	320 - 355	3709.0
3	99 - 138	4662.3
8	261 - 319	6794.6
7	179 - 260	9284.3
2	2 - 98	10881.4

**Table IV-Cleavage of MLSK-1 with cyanogen bromide**

Position	From-To	Molecular Weight
1	1 - 1	149.2
4	109 - 133	2815.3
2	2 - 39	3888.4
6	253 - 289	4182.8
7	290 - 336	5186.6
8	337 - 387	5736.5
3	40 - 108	8283.6
5	134 - 252	13554.3
9	388 - 631	26152.9

**Table V-Cleavage of MLSK-2 with cyanogen bromide**

Position	From-To	Molecular Weight
1	1 - 1	149.2
6	181 - 184	446.5
5	165 - 180	1915.2
3	92 - 118	3149.7
8	265 - 311	5276.8
4	119 - 164	5279.1
7	185 - 264	9036.3
2	2 - 91	10174.7

5

**Table VI-Cleavage of LNRK-1 with cyanogen bromide**

Position	From-To	Molecular Weight
11	285 - 431	18345.0

17	824 - 879	5992.1
12	432 - 525	12060.5
3	57 - 72	1879.0
13	526 - 551	2971.3
25	1253 - 1254	278.3
20	958 - 965	858.9
1	1 - 1	149.2
31	1358 - 1358	149.2
30	1351 - 1357	834.9
19	905 - 957	5627.1
9	237 - 239	383.5
32	1359 - 1360	318.3
18	880 - 904	2576.8
8	227 - 236	1003.1
22	1070 - 1091	2693.1
5	98 - 105	1019.2
27	1283 - 1295	1460.7
28	1296 - 1317	2431.7
29	1318 - 1350	3877.5
26	1255 - 1282	3280.7
14	552 - 584	3584.0
4	73 - 97	2935.4
15	585 - 635	5487.2
7	196 - 226	3415.7
16	636 - 823	20422.3
2	2 - 56	5858.6
10	240 - 284	5311.2
21	966 - 1069	11599.8
6	106 - 195	10251.7
24	1181 - 1252	7943.0
23	1092 - 1180	10501.4

In addition, the preferred purified polypeptide of the invention (SEQ ID NOs:8-14) have calculated molecular weights in the absence of glycosylation as follows:

Table VII

Polypeptide	Daltons
MDCK-1 (SEQ ID NO:8)	$M_r \sim 34,813$ and
MDCK-2 (SEQ ID NO:9)	$M_r \sim 34,537$ (from MET 3) $M_r \sim 33,761$ (from MET 10) $M_r \sim 31,740$ (from MET 28)
MDCK-3 (SEQ ID NO:10)	$M_r \sim 39,947$
MLSK-1 (SEQ ID NO:11)	$M_r \sim 69,806$
MLSK-2 (SEQ ID NO:13)	$M_r \sim 39,477$
SS4694 (SEQ ID NO:13)	$M_r \sim 29,954$
LNK-1 (SEQ ID NO:14)	$M_r \sim 154,943$

- 5 Finally, as to the kits that are encompassed by the invention, the constituents of such kits can be varied, but typically contain the polypeptide and fragmented peptide molecular weight markers. Also, such kits can contain the polypeptides wherein a site necessary for fragmentation has been removed. Furthermore, the kits can contain reagents for the specific cleavage of the polypeptide and the unknown protein by chemical or enzymatic cleavage.
- 10 Kits can further contain antibodies directed against polypeptides or fragments thereof of the invention.

#### Identification of Unknown Proteins

- As set forth above, a polypeptide or peptide fingerprint can be entered into or
- 15 compared to a database of known proteins to assist in the identification of the unknown protein using mass spectrometry (W.J. Henzel et al., Proc. Natl. Acad. Sci. USA 90:5011-5015, 1993; D. Fenyo et al., Electrophoresis 19:998-1005, 1998). A variety of computer software programs to facilitate these comparisons are accessible via the Internet, such as Protein Prospector (Internet site: [prospector.uscf.edu](http://prospector.uscf.edu)), MultiIdent (Internet site: [www.expasy.ch/sprot/multiident.html](http://www.expasy.ch/sprot/multiident.html)), PeptideSearch (Internet site: [www.mann.embl-](http://www.mann.embl-)
- 20

heidelberg.de...deSearch/FR\_PeptideSearch Form.html), and ProFound (Internet site: www.chait-sgi.rockefeller.edu/cgi-bin/ prot-id-frag.html). These programs allow the user to specify the cleavage agent and the molecular weights of the fragmented peptides within a designated tolerance. The programs compare observed molecular weights to predicted peptide molecular weights derived from sequence databases to assist in determining the identity of the unknown protein.

In addition, a polypeptide or peptide digest can be sequenced using tandem mass spectrometry (MS/MS) and the resulting sequence searched against databases (J.K. Eng, et al., J. Am. Soc. Mass Spec. 5:976-989 (1994); M. Mann and M. Wilm, Anal. Chem. 66:4390-4399 (1994); J.A. Taylor and R.S. Johnson, Rapid Comm. Mass Spec.11:1067-1075 (1997)). Searching programs that can be used in this process exist on the Internet, such as Lutefisk 97 (Internet site: www.lsbcc.com:70/Lutefisk97.html), and the Protein Prospector, Peptide Search and ProFound programs described above.

Therefore, adding the sequence of a gene and its predicted protein sequence and peptide fragments to a sequence database can aid in the identification of unknown proteins using mass spectrometry.

### Antibodies

Antibodies that are immunoreactive with the polypeptides of the invention are provided herein. Such antibodies specifically bind to the polypeptides *via* the antigen-binding sites of the antibody (as opposed to non-specific binding). Thus, the polypeptides, fragments, variants, fusion proteins, etc., as set forth above may be employed as "immunogens" in producing antibodies immunoreactive therewith. More specifically, the polypeptides, fragment, variants, fusion proteins, etc. contain antigenic determinants or epitopes that elicit the formation of antibodies.

These antigenic determinants or epitopes can be either linear or conformational (discontinuous). Linear epitopes are composed of a single section of amino acids of the polypeptide, while conformational or discontinuous epitopes are composed of amino acids sections from different regions of the polypeptide chain that are brought into close proximity upon protein folding (C. A. Janeway, Jr. and P. Travers, *Immuno Biology* 3:9 (Garland Publishing Inc., 2nd ed. 1996)). Because folded proteins have complex surfaces, the number of epitopes available is quite numerous; however, due to the conformation of the protein and

steric hinderances, the number of antibodies that actually bind to the epitopes is less than the number of available epitopes (C. A. Janeway, Jr. and P. Travers, *Immuno Biology* 2:14 (Garland Publishing Inc., 2nd ed. 1996)). Epitopes may be identified by any of the methods known in the art.

5           Thus, one aspect of the present invention relates to the antigenic epitopes of the polypeptides of the invention. Such epitopes are useful for raising antibodies, in particular monoclonal antibodies, as described in more detail below. Additionally, epitopes from the polypeptides of the invention can be used as research reagents, in assays, and to purify specific binding antibodies from substances such as polyclonal sera or supernatants from  
10       cultured hybridomas. Such epitopes or variants thereof can be produced using techniques well known in the art such as solid-phase synthesis, chemical or enzymatic cleavage of a polypeptide, or using recombinant DNA technology.

          As to the antibodies that can be elicited by the epitopes of the polypeptides of the invention, whether the epitopes have been isolated or remain part of the polypeptides, both  
15       polyclonal and monoclonal antibodies may be prepared by conventional techniques. See, for example, *Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses*, Kennet et al. (eds.), Plenum Press, New York (1980); and *Antibodies: A Laboratory Manual*, Harlow and Land (eds.), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, (1988).

20       Hybridoma cell lines that produce monoclonal antibodies specific for the polypeptides of the invention are also contemplated herein. Such hybridomas may be produced and identified by conventional techniques. One method for producing such a hybridoma cell line comprises immunizing an animal with a polypeptide; harvesting spleen cells from the immunized animal; fusing said spleen cells to a myeloma cell line, thereby  
25       generating hybridoma cells; and identifying a hybridoma cell line that produces a monoclonal antibody that binds the polypeptide. The monoclonal antibodies may be recovered by conventional techniques.

          The monoclonal antibodies of the present invention include chimeric antibodies, e.g., humanized versions of murine monoclonal antibodies. Such humanized antibodies may be  
30       prepared by known techniques and offer the advantage of reduced immunogenicity when the antibodies are administered to humans. In one embodiment, a humanized monoclonal antibody comprises the variable region of a murine antibody (or just the antigen binding site



thereof) and a constant region derived from a human antibody. Alternatively, a humanized antibody fragment may comprise the antigen binding site of a murine monoclonal antibody and a variable region fragment (lacking the antigen-binding site) derived from a human antibody. Procedures for the production of chimeric and further engineered monoclonal antibodies include those described in Riechmann et al. (*Nature* 332:323, 1988), Liu et al. (*PNAS* 84:3439, 1987), Larrick et al. (*Bio/Technology* 7:934, 1989), and Winter and Harris (*TIPS* 14:139, May, 1993). Procedures to generate antibodies transgenically can be found in GB 2,272,440, US Patent Nos. 5,569,825 and 5,545,806 and related patents claiming priority therefrom, all of which are incorporated by reference herein.

Antigen-binding fragments of the antibodies, which may be produced by conventional techniques, are also encompassed by the present invention. Examples of such fragments include, but are not limited to, Fab and F(ab')<sub>2</sub> fragments. Antibody fragments and derivatives produced by genetic engineering techniques are also provided.

In one embodiment, the antibodies are specific for the polypeptides of the present invention and do not cross-react with other proteins. Screening procedures by which such antibodies may be identified are well known, and may involve immunoaffinity chromatography, for example.

#### Uses Thereof

The antibodies of the invention can be used in assays to detect the presence of the polypeptides or fragments of the invention, either *in vitro* or *in vivo*. The antibodies also may be employed in purifying polypeptides or fragments of the invention by immunoaffinity chromatography.

Those antibodies that additionally can block binding of the polypeptides of the invention to a binding partner may be used to inhibit a biological activity that results from such binding. Such blocking antibodies may be identified using any suitable assay procedure, such as by testing antibodies for the ability to inhibit binding of kinases of the invention to the binding partner. Alternatively, blocking antibodies may be identified in assays for the ability to inhibit a biological effect that results from binding of kinases to binding partners.

Such an antibody may be employed in an *in vitro* procedure, or administered *in vivo* to inhibit a biological activity mediated by the entity that generated the antibody. Disorders caused or exacerbated (directly or indirectly) by the interaction of kinases with binding

partners thus may be treated. A therapeutic method involves *in vivo* administration of a blocking antibody to a mammal in an amount effective in inhibiting a binding partner-mediated biological activity. Monoclonal antibodies are generally preferred for use in such therapeutic methods. In one embodiment, an antigen-binding antibody fragment is employed.

5       Antibodies may be screened for agonistic (*i.e.*, ligand-mimicking) properties. Such antibodies, upon binding to a binding partner, induce biological effects (e.g., transduction of biological signals) similar to the biological effects induced when the kinases of the invention bind to binding partners.

10       Compositions comprising an anti-kinase antibody, and a physiologically acceptable diluent, excipient, or carrier, are provided herein. Suitable components of such compositions are as described above for compositions containing kinase proteins.

Also provided herein are conjugates comprising a detectable (e.g., diagnostic) or therapeutic agent, attached to the antibody. Examples of such agents are presented above. The conjugates find use in *in vitro* or *in vivo* procedures.

15

#### Therapeutic Activities

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the therapeutic uses or biological activities (including those associated with assays cited herein) identified below. Therapeutic uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by  
20       administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

#### Cytokine and Cell Proliferation/Differentiation Activity

25       A protein of the present invention may exhibit cytokine-inducing, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce or inhibit production of cytokines in certain cell populations. The cell-proliferation activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without  
30       limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK. The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-

cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994. Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon .gamma., Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994. Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6-Nordan, R. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9-Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

#### Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and

disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high

level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign  
5 by T cells, followed by an immune reaction that destroys the transplant. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of  
10 immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

15 Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to  
20 isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express the protein, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or enhancement of antigen function (preferably  
25 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. The transfected tumor cells are returned  
30 to the patient to result in expression of the peptides in the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The activity of a protein of the invention may, among other means, be measured by

the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte

5 Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. U.S.A. 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. U.S.A. 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et

10 al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994. Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent

15 antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994. Mixed lymphocyte reaction (MLR) assays (which will identify, among others,

20 proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai

25 et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador

30 et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical

Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. U.S.A. 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal

hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

5       The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above. Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151,  
10       1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993. Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc.,  
15       New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. U.S.A. 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of  
20       Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-  
25       162, Wiley-Liss, Inc., New York, N.Y. 1994.

#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for  
30       wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers. A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone



fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery. A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes. Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and

peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like. It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity. A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above. The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. W095/16035 (bone, cartilage, tendon); International Patent Publication No. W095/05846 (nerve, neuronal); International Patent Publication No. W091/07491 (skin, endothelium). Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

### Inflammation

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

### Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

### Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height,

weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### Administration and Dosing

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration.

The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or complement its activity or use in treatment. Such additional factors

and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form. The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Pat. No. 4,235,871; U.S. Pat. No. 4,501,728; U.S. Pat. No. 4,837,028; and U.S. Pat. No. 4,737,323, all of which are incorporated herein by reference. As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a

meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to  
5 combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance  
10 with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or  
15 sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors. Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety  
20 of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule,  
25 powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as  
30 peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or

polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

5 When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition  
10 to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

15 The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of  
20 protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 .mu.g to about 100 mg (preferably about 0.1 ng to about 10 mg,  
25 more preferably about 0.1 .mu.g to about 1 mg) of protein of the present invention per kg body weight. The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the  
30 range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are  
5 conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J. L. Krstenansky, et al., FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein  
10 may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

15 For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or  
20 injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention.  
25 Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications. The choice of matrix material is based on  
30 biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically



defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix. A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF). The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be

used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling. Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

The following examples are provided to further illustrate particular embodiments of the invention, and are not to be construed as limiting the scope of the present invention.

#### **EXAMPLE 1: Isolation of Polynucleotides Encoding Novel Kinases**

High through put sequencing of murine dendritic cell, murine lymph node stromal cell, and human dendritic cell libraries generated nucleotide sequences which were used to query public and private sequence databases using an algorithm designed to recognize kinase subdomains. Putative kinase clones identified in this manner were further sequenced. The resultant complete clone sequences are shown as: SEQ ID NO:1-6, and Table VIII identifies the specific library and clones for each of these sequences. In the case of SS4694 (SEQ ID NO:6), sequence information derived from SS4694 and KIAA0551 (see pp. 11/26-27) enabled the cloning of LNRK-1 (SEQ ID NO:7) from a Marathon-ready human spleen cDNA library (Clontech).

**Table VIII**

Name	SEQ ID NO	Library	Clone #
MDCK-1	1	Murine dendritic cell	990219MDCA001250HT
MDCK-2	2	Murine dendritic cell	990205MDCA999084HT
MDCK-3	3	Murine dendritic cell	990217MDCA001428HT
MLSK-1	4	Murine lymph node stromal cell	980906MLSA002022HT
MLSK-2	5	Murine lymph node stromal cell	9980905MLSA001070HT
LNK-1	6	Human dendritic cell	ss4694

**EXAMPLE 2 Use of kinase polypeptides in an ELISA****Kinase-specific ELISA:**

5            Serial dilutions of kinase-containing samples (in 50 mM NaHCO<sub>3</sub>, brought to pH 9 with NaOH) are coated onto Linbro/Titertek 96 well flat bottom E.I.A. microtitration plates (ICN Biomedicals Inc., Aurora, OH) at 100:1/well. After incubation at 4°C for 16 hours, the wells are washed six times with 200:1 PBS containing 0.05% Tween-20 (PBS-Tween). The wells are then incubated with FLAG®-binding partner at 1 mg/ml in PBS-Tween with 5% fetal calf serum (FCS) for 90 minutes (100:1 per well), followed by washing as above. Next, each well is incubated with the anti-FLAG® (monoclonal antibody M2 at 1 mg/ml in PBS-Tween containing 5% FCS for 90 minutes (100:1 per well), followed by washing as above. Subsequently, wells are incubated with a polyclonal goat anti-mIgG1-specific horseradish peroxidase-conjugated antibody (a 1:5000 dilution of the commercial stock in PBS-Tween containing 5% FCS) for 90 minutes (100:1 per well). The HRP-conjugated antibody is obtained from Southern Biotechnology Associates, Inc., Birmingham, Alabama. Wells then are washed six times, as above.

For development of the ELISA, a substrate mix [100:1 per well of a 1:1 premix of the TMB Peroxidase Substrate and Peroxidase Solution B (Kirkegaard Perry Laboratories, Gaithersburg, Maryland)] is added to the wells. After sufficient color reaction, the enzymatic reaction is terminated by addition of 2 N H<sub>2</sub>SO<sub>4</sub> (50 :1 per well). Color intensity (indicating kinase/binding partner binding activity) is determined by measuring extinction at 450 nm on a V Max plate reader (Molecular Devices, Sunnyvale, CA).

**EXAMPLE 3: Monoclonal Antibodies That Bind**

This example illustrates a method for preparing monoclonal antibodies that bind kinases of the invention. Suitable immunogens that may be employed in generating such antibodies include, but are not limited to, purified kinase polypeptides or an immunogenic  
5 fragment thereof, or fusion proteins containing a kinase of the invention (e.g., a soluble kinase/Fc fusion protein).

Purified kinases can be used to generate monoclonal antibodies immunoreactive therewith, using conventional techniques such as those described in U.S. Patent 4,411,993.  
10 Briefly, mice are immunized with kinase immunogen emulsified in complete Freund's adjuvant, and injected in amounts ranging from 10-100 µg subcutaneously or intraperitoneally. Ten to twelve days later, the immunized animals are boosted with additional kinase immunogen emulsified in incomplete Freund's adjuvant. Mice are periodically boosted thereafter on a weekly to bi-weekly immunization schedule. Serum  
15 samples are periodically taken by retro-orbital bleeding or tail-tip excision to test for anti-kinase antibodies by dot blot assay, ELISA (Enzyme-Linked Immunosorbent Assay) or inhibition of kinase/binding partner binding.

Following detection of an appropriate antibody titer, positive animals are provided one last intravenous injection of kinase immunogen in saline. Three to four days later, the  
20 animals are sacrificed, spleen cells harvested, and spleen cells are fused to a murine myeloma cell line, e.g., NS1 or preferably P3x63Ag8.653 (ATCC CRL 1580). Fusions generate hybridoma cells, which are plated in multiple microtiter plates in a HAT (hypoxanthine, aminopterin and thymidine) selective medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

25 The hybridoma cells are screened by ELISA for reactivity against purified kinase polypeptides by adaptations of the techniques disclosed in Engvall et al., *Immunochem.* 8:871, 1971 and in U.S. Patent 4,703,004. A preferred screening technique is the antibody capture technique described in Beckmann et al., (*J. Immunol.* 144:4212, 1990) Positive hybridoma cells can be injected intraperitoneally into syngeneic BALB/c mice to produce  
30 ascites containing high concentrations of anti-kinase monoclonal antibodies. Alternatively, hybridoma cells can be grown *in vitro* in flasks or roller bottles by various techniques. Monoclonal antibodies produced in mouse ascites can be purified by ammonium sulfate

precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to Protein A or Protein G can also be used, as can affinity chromatography based upon binding to kinase polypeptides of the invention.

5 **EXAMPLE 4: PCR Analysis of Tissue-Specific Kinase Expression**

The tissue distribution of MDCK-2, MDCK-3, MLSK-1, MLSK-2 and ss4694 mRNA was investigated. Using Clontech multiple tissue cDNA panels and clone specific oligonucleotide PCR primers, we determined that expression of MDCK-2 was ubiquitous throughout the Clontech murine cDNA panel, with highest levels in spleen, liver, skeletal  
10 muscle and seven day embryo. MDCK-3 expression was highest in heart, brain and spleen; lower level expression was seen in liver, skeletal muscle and testis, and low but detectable levels in lung and kidney. Expression of MLSK-1 was found to be highest in the heart, lung, and liver.

Lower levels of MLSK-1 were detected in the kidney and skeletal muscle, and  
15 MLSK-1 expression was absent from brain and spleen. Expression of MLSK-2 was highest in the heart and spleen while lower levels of expression were found in the lung and liver, and no expression was detectable in the brain, skeletal muscle, kidney and testis.

SS4694 and therefore LNRK-1 expression is ubiquitous throughout the human cDNA panels (Clontech human tissue panel 1, human tissue panel 2 and human immune tissue  
20 panel) with highest levels in peripheral blood lymphocyte cDNA. All other tissues had roughly equivalent levels of expression.

**EXAMPLE 5: Measuring kinase activity**

Isolated kinase polypeptides or fusion proteins containing the isolated protein kinase  
25 domain can be used in an assay of protein kinase activity.

Typically this would be carried out by combining a kinase of the invention with radiolabeled ATP ( $\gamma^{32}\text{P}$ -ATP) and a magnesium (or other divalent cation, such as manganese) salt in buffer solution containing a peptide or protein substrate. Peptide substrates are generally from 8-30 amino acids in length and may terminate at the N- or C-terminus with  
30 three or more lysine or arginine residues to facilitate binding of the peptide to phosphocellulose paper. The substrate may also be a protein known to be phosphorylated readily by a kinase of the invention. Many such general kinase substrates are known, such

as,  $\alpha$  or  $\beta$  casein, histone H1, myelin basic protein, etc. After incubation of this reaction mixture at 20-37°C for a suitable time, the transfer of radioactive phosphate from ATP to the substrate protein or substrate peptide may be monitored, by acidifying the reaction mixture then spotting it onto phosphocellulose paper, and subsequent washing of the paper with a dilute solution of phosphoric acid, in the case of a peptide substrate, or by application of the reaction products to a gel electrophoresis system followed by autoradiographic detection in the case of proteins.

A specific example of this type of assay of kinase activity is the PhosphoSpots™ assay (Jerini Bio Tools GMBH), in which protein or peptide substrates are attached to a solid support. In one example, the substrates may be peptides where each is known to be phosphorylated by a particular kinase. When the kinase being tested is added to the substrates in the presence of  $\gamma$ -<sup>32</sup>P, any attached proteins or peptides that are suitable substrates for that kinase will be labeled with the  $\gamma$ -<sup>32</sup>P which can be quantitatively detected using a phosphoimager. (See, for example, Tegge *et al.*, 1995, Determination of cyclic nucleotide-dependent protein kinase substrate specificity by the use of peptide libraries on cellulose paper, *Biochemistry* 34 (33): 10569-10577, which is incorporated by reference herein). The results of such an assay for MLSK-1 substrate specificity are shown in Table IX below.

**Table IX. Phosphorylation of known kinase substrates by MLSK-1**

Protein Kinase ("PK")	Known PK Substrate Sequence	Phosphorylation by MLSK-1 (% of max.)
cAMP-dependent protein kinase	LRRASLG	65.9
cGMP-dependent protein kinase	RKISASEFDRPLR	62.2
protein kinase C	KKRFSFKKSFKLSGFSEFK	100.0
protein kinase C	QKRPSQRSK	75.0
Ca-/calmodulin-dependent PK	KKALRRQETVDAL	20.9
Ca-/calmodulin-dependent PK	PLARTLSVAGLPGK	10.3
casein kinase II	RRRDDDSDDD	17.6
cdc2-kinase	Ac-SPGRRRRK	94.8
p34 cdc-kinase	PKTPKKAKKL	82.0
p42/p44 MAP kinase	APRTPGRR	88.6
p42/p44 MAP kinase	EAAEAEPAPSSPAEAEGA	0.0
p42/p44 MAP kinase	LMECRNSPVAKT	3.8
casein kinase I	RRKDLHDDEEDEAMSITA	14.1
S6 kinase	LSSLRASTKSGGQK	66.6
myosin light chain kinase	KKRPQRATSNVFS	72.0

insulin receptor tyrosine kinase	KKKLDPATGDYMNMSVGD	33.7
csk tyrosine kinase	KKKKKEEYFFF	82.1
raf-1 kinase	SGQLDSMANSFVGTRS	43.1
abl tyrosine kinase	EAIYAAPFAKKK	69.3
c-src tyrosine kinase	YTYGSFK	66.6

Kinase activity may also be measured, *in vitro* or in intact cells, using a fluorescence resonance energy transfer (FRET) assay, in which the transfer of energy between fluorescently tagged kinase and substrate molecules is detected. (For example, see Ng *et al.*,  
5 1999, Imaging protein kinase C alpha activation in cells, *Science* **283** (5410): 2085-2089, which is incorporated by reference herein.)

Other methods are available to conveniently measure the kinase-mediated transfer of phosphate to substrate proteins or peptides, such as the scintillation proximity assay, and the use of monoclonal antibodies that are specific for phosphorylated or non-phosphorylated  
10 forms of substrate molecules; these methods are well known to those practiced in the art.

#### **EXAMPLE 6: Tissue- and Stage-Specific Expression of Kinase mRNAs**

The expression of MDCK-2, MDCK-3, MLSK-1, MLSK-2, and ss4694 (LNRK-1) was assessed by PCR using gene-specific oligonucleotide primers directed toward these  
15 kinase-encoding polynucleotides using Clontech multiple tissue cDNA panels as templates. Expression of MDCK-2, MDCK-3, MLSK-1, and MLSK-2 was assayed using the murine cDNA panel (see Table X below). Expression of MDCK-2 was observed in all tissues on this panel, with the highest levels in spleen, liver, skeletal muscle, and seven-day embryo. Expression of MDCK-3 was highest in heart, brain and spleen; lower-level expression was  
20 seen in liver, skeletal muscle and testis, and low but detectable levels were observed in lung and kidney; however, expression of MDCK-3 was completely absent from murine embryo. Expression of MLSK-1 was highest in the heart, lung, and liver, and is absent from the brain and spleen; MLSK-1 expression in the embryo is only seen at the 11-day stage. Expression of MLSK-2 is found to be highest in the heart and spleen. MLSK-2 is expressed at lower  
25 levels in lung, liver, and 7-day embryo, and is not detectable in brain, skeletal muscle, kidney, testis, or embryonic tissue at other stages of development. ss4694(LNRK-1) expression is ubiquitous throughout the human cDNA panels, with highest levels in PBL (peripheral blood lymphocyte) cDNA. All other tissues had roughly equivalent levels of expression.

**Table X**

MURINE PANEL	MDCK-2	MDCK-3	MLSK-1	MLSK-2
Heart	**	***	***	***
Brain	**	***		
Spleen	***	***		**
Lung	**	*	***	*
Liver	***	**	***	*
Skeletal Muscle	***	**	*	
Kidney	**	*	**	
Testis	**	**		
7-day Embryo	***			*
11-day Embryo	**		**	
15-day Embryo	*			
17-day Embryo	**			

- Expression of the ss4694 clone (and therefore of LNRK-1) was assayed using the
- 5 Clontech "human tissue" and "human immune" cDNA panels (see Table XI below). ss4694 (LNRK-1) expression is observed throughout the human cDNA panels, with highest levels in PBL (peripheral blood lymphocyte) cDNA. All other tissues had roughly equivalent levels of expression.

10 **Table XI**

HUMAN TISSUE PANEL I	ss4694 / LNRK-1 Expression
Brain	**
Heart	**
Kidney	*
Liver	**
Lung	**
Pancreas	**
Placenta	**
Skeletal Muscle	*
HUMAN TISSUE PANEL II	
Colon	**
Ovary	**
PBL	***
Prostate	**
Small Intestine	*
Spleen	**
Testis	**
Thymus	**
HUMAN IMMUNE PANEL	
Bone Marrow	**
Fetal Liver	**
Lymph Node	**
PBL	***
Spleen	**
Thymus	**
Tonsil	**



**EXAMPLE 7: Regulation of MDCK-3 Expression in Dendritic Cell Maturation**

The regulation of MDCK-3 RNA expression during dendritic cell "maturation" and/or "activation" was assayed by RT (reverse transcriptase) PCR (polymerase chain reaction). Flt3 ligand ("Flt3L") is a growth factor that stimulates the proliferation of hematopoietic cells. RNA samples isolated from splenic dendritic cells purified from Flt3L-treated mice were assayed by RT PCR using primers derived from the MDCK-3 cDNA sequence. MDCK-3 RNA was undetected in the freshly isolated dendritic cells, but was present in cells following overnight culture in a defined medium, a growth procedure which causes dendritic cell "maturation". This indicates that regulation of MDCK-3 expression is correlated with the maturation state of at least one type of cell involved in immune responses.

Furthermore, RT PCR was performed on RNA isolated from a different dendritic cell system, where murine bone marrow cells are isolated and then cultured in media containing Flt3 ligand for nine days, with the addition of various dendritic cell "activators" during the final 24 hours of the incubation period. MDCK-3 mRNA levels were specifically altered by some "activators" but not others.

These assays can also be performed with a variety of cells such as peripheral blood mononuclear cells and a variety of activating substances such as IL-4, GM-CSF, TNF, IL-2, IFN, LPS, etc. to test for a correlation between changes in cell differentiation or proliferative activity and the expression of the kinases of the invention.

**EXAMPLE 8: Assaying Activation of Kinase Pathways by Detecting Phosphorylation of Known Pathway Components**

Cell signalling pathways often involve a cascade of phosphorylation events. Over-expression of kinases in cells can activate such signalling pathways, and this activation may be detected by measuring the level of phosphorylation of molecules that are known to be 'downstream' phosphorylated recipients of 'upstream' kinase activity. Conversely, over-expression of a catalytically inactive, truncated, or otherwise mutated form of a kinase can act as a dominant negative mutation and disrupt or abolish normal signalling events 'downstream' of the kinase.

In one example, we expressed active forms of MLCK-1 and of MLCK-2 and showed that when over-expressed in COS cells each of these kinases activates the MAP kinase

signaling pathway as evidenced by the generation of phosphorylated forms of ERK, a 'downstream' kinase in the MAP kinase pathway. Phosphorylation of signalling pathway molecules can be detected in a variety of ways, including incorporation of  $^{32}\text{P}$  followed by immunoprecipitation, FRET assays as described in Example 5, or the use of phosphorylation-state-specific antibodies in ELISA assays or on Western blots. Additionally, kinase specificity for a particular cell signalling pathway can be assessed by comparing the phosphorylation responses of 'downstream' molecules in different pathways to over-expression of that kinase. For example, over-expression of MLSK-1 and of MLSK-2 in COS cells had no effect on the stress-activated kinase pathway, as expression of these kinases did not result in activation of either JNK or p38 kinases.

#### **EXAMPLE 9: Reporter Gene Assays of Kinase Pathway Activation**

Activation of cell signalling pathways by kinases of the invention may also be assayed using reporter gene constructs. In such constructs a reporter gene such as luciferase or  $\beta$ -galactosidase is placed downstream of a promoter, enhancer, or other transcriptional regulatory element that is known to bind transcription factors as a result of activation of a cell signalling pathway. This transcriptional regulatory element may be selected on the basis of its known association with a relevant transcription factor, such as AP-1 or NF $\kappa$ B, or on the basis of physical association with a downstream gene known to be regulated by the signalling pathway. An example of the use of such reporter constructs is described in Ling *et al.*, 1998, NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176, *Proc Natl Acad Sci USA* **95** (7): 3792-3797, which is incorporated by reference herein.

In one example, assays to determine whether MLSK-1 or MLSK-2 could activate the transcription factor AP-1 were performed. AP-1 is a transcription factor known to be involved in the JNK and p38 signalling pathways. MLSK-1 and MLSK-2 were each individually co-transfected with an AP-1-luciferase construct into COS-7 cells in a standard AP-1-luciferase reporter assay. The overexpression of neither MLSK-1 nor MLSK-2 activates AP-1 using this assay system, consistent with these kinases not participating in the stress-activated JNK and p38 signalling pathways.

The specification is most thoroughly understood in light of the teachings of the references cited within the specification which are hereby incorporated by reference. The

embodiments within the specification provide an illustration of embodiments of the invention and should not be construed to limit the scope of the invention. The skilled artisan readily recognizes that many other embodiments are encompassed by the invention.

What is claimed is:

1. An isolated nucleic acid molecule selected from the group consisting of:
  - (a) the DNA sequence of SEQ ID NOs:1-7;
  - (b) an isolated nucleic acid molecule encoding an amino acid sequence comprising the sequence of SEQ ID NOs:8-14;
  - (c) an isolated nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of (a) or (b) under conditions of moderate stringency in 50% formamide and 6XSSC, at 42°C with washing conditions of 60°C, 0.5XSSC, 0.1% SDS;
  - (d) an isolated nucleic acid molecule derived by *in vitro* mutagenesis from SEQ ID NOs:1-7;
  - (e) an isolated nucleic acid molecule degenerate from SEQ ID NOs:1-7 as a result of the genetic code; and
  - (f) an isolated nucleic acid molecule that is at least 80% identical to any of (a)-(e).
2. A recombinant vector that directs the expression of the nucleic acid molecule of claim 1.
3. An isolated polypeptide encoded by the nucleic acid molecule of claim 1.
4. An isolated polypeptide according to claim 3 in non-glycosylated form.
5. Isolated antibodies that bind to a polypeptide of claim 3.
6. Isolated antibodies according to claim 5, wherein the antibodies are monoclonal antibodies.
7. A host cell transfected or transduced with the vector of claim 2.

8. A method for the production of kinase polypeptide comprising culturing a host cell of claim 2 under conditions promoting expression, and recovering the polypeptide from the culture medium.

9. The method of claim 8, wherein the host cell is selected from the group consisting of bacterial cells, yeast cells, plant cells, insect cells and animal cells.

10. An isolated kinase polypeptide comprising an amino acid sequence selected from the group consisting of:

- (a) amino acids 1-275, 25-275, 140-226, or 149-175 of SEQ ID NO:8;
- (b) amino acids 1-302, 8-302, 26-302, 34-295, 60-229, 157-183, or 198-229 of SEQ ID NO:9;
- (c) amino acids 1-355, 23-279, 124-221, 134-169, or 183-214 of SEQ ID NO:10;
- (d) amino acids 1-631, 57-309, 129-254, 175-200, or 215-247 of SEQ ID NO:11;
- (e) amino acids 1-311, 14-271, 41-213, 124-161, or 175-206 of SEQ ID NO:12;
- (f) amino acids 1-266, 1-261, 25-258, 101-233, 149-175, or 190-226 of SEQ ID NO:13;
- (g) amino acids 1-1360, 25-306, 25-258, 101-233, 149-175, or 190-226 of SEQ ID NO:14;
- (h) an amino acid sequence that is at least 80% identical to any of the amino acid sequences of (a) – (g) above.

11. A method of designing an inhibitor of the polypeptide of claim 10, the method comprising the steps of determining the three-dimensional structure of such polypeptide, analyzing the three-dimensional structure for the likely binding sites of substrates, synthesizing a molecule that incorporates a predicted reactive site, and determining the polypeptide-inhibiting activity of the molecule.

12. A method for identifying compounds that inhibit kinase activity comprising:
- (a) bringing a test compound into contact with the polypeptide of claim 10 and a substrate; and
  - (b) determining whether the test compound inhibits the kinase activity of said polypeptide.

13. A method for identifying compounds that activate kinase activity comprising:
  - (a) bringing a test compound into contact with the polypeptide of claim 10 and a substrate; and
  - (b) determining whether the test compound activates the kinase activity of said polypeptide.
14. The method of claim 12 where the test compound is brought into contact with the polypeptide in a cell containing at least one recombinant vector that directs the expression of at least one polynucleotide encoding said polypeptide.
15. The method of claim 13 where the test compound is brought into contact with the polypeptide in a cell containing at least one recombinant vector that directs the expression of at least one polynucleotide encoding said polypeptide.
16. A method for inhibiting the kinase activity of the polypeptide of claim 10 comprising forming a mixture of the polypeptide of claim 10, a substrate, and a compound, wherein the compound blocks the binding of the polypeptide of claim 10 with the substrate.



**MDCK-2**

MDEQSQGMQGPVPTQFQPKALRPDMGYNTLANFRIEKKIGRGQFSEVYRASCLLDGV  
 |                   |   |   |   |  
  o               og G g v

PVALKKVQIFDLMDAKARADCIKEIDLLKQLNHPNVIKYYASFIEDNELNIVLELADAGD  
 | | | | |                   |   |   |   |   |   |   |   |   |   |  
 oaoK o                   E oo h oo o o               oooo\*oo

LSRMIKHFFKKQKRLIPERTVWKYFVQLCSALDHMHSRRVMHRDIKPANVFITATGVVKLG  
          |               |           |   \*o   +ooh               | | | | | | | | | |  
          o               o           o           oohrDok   Nooo               oko+

DLGLGRFFSSKTTAAHSLVGTPYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYG  
 | | | | |                   | |   |   | | | | |               | | | | | | | | | |  
 Dfgo+                   g+ o +pEoo               o               Doo+ogoooo o               po

DKMNLVSLCKKIEQCDYPPPLPSDHYSEELRQLVNICINPDPEKRPDIAYVYDVAKRMHAC  
          | |   |               |                   | |   | |               | |               |  
          oo o               o                   oo oo               R +               o

TAST

**FIGURE 2**



### MDCK-3

MARENGESSSSWKQAEDIKKIFEKFKETLGTGAFSEVVLAEEKATGKLF  
 | | | | | | | | | |  
 o og G og v oa

VKCIPKKALKKGKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVMQL  
 | | | | | | | | | |  
 OK o E o h oo o o

VSGGELFDRIVEKGFYTEKDASTLIRQVLDAVYYLHRMGIVHRDLKPENL  
 | | | | | | | | | |  
 o o \*o +o ooh oo hrDoK+ No

LYYSQDEESKIMISDFGLSKMEGKGDVMSTACGTPGYVAPEVLAQKPYSK  
 | | | | | | | | | |  
 oo oko+Dfgo+ g+ o +pEoo o

AVDCWSIGVIAIYILLCGYPFFYDENDSKLFEQILKAIEYEFDSPYWDDISD  
 | | | | | | | | | |  
 Doo+ogoooo o po oo o o

SAKDFIRNLMKEDPNKRYTCEQAARHPWIAGDTALSKNIHESVSAQIRKN  
 | | | | | | | | | |  
 oo oo R + o

FAKSKWRQAFNATAVVRHMRRLQLGSSLDSSNASVSSNLSLASQKDCASG  
 TFHAL

**MLSK-1**[illegible]

**FIGURE 4**

## MLSK-2

MAGPSWGLPRLDGFILTERLGSGTYATVYKAYAKKDTREVVAIKCVAKKSLNKASVENLLT  
                           |          |||  |  |                          |||  |  |  
                           o          og  G  g  v                          oaoK  o

EIEILKGIRHPHIVQLKDFQWDNDNIYLIMEFCAGGDLRSFIHTRRILPEKVARVFMQQLA  
 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  
 E  oo  h  oo  o  o          oooooooo\*oo          o  o  o          o  \*o

SALQFLHERNISHLDLKPQNILLSSLEKPHLKLADFGFAQHMSPWDEKHVLRGSPLYMAPE  
 ||  ||  |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  
 +o  ooh  oohrDok+  Nooo          oko+Dfgo+          g+  o  +pE

MVCRRQYDARVDLWSVGVIYEALEFGQPPFASRSFSELEEKIRSNRVIEVRLAGSRHPPGI  
 ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  
 oo  o  Doo+ogoooo-o          po          oo  o          o          oo

EGLKAQKFVQHCSAGSGRFMAVGHVLLWVKPRVWSVPEDPYQPRQATNDQAQSSHSPGLEAN  
 |                          |  |          |  
 oo                          R  +          o

THLIGD

FIGURE 5

MASDSPARSLDEIDL SALRDPAGIFELVELVNGTYGQVYKGRHVKTGQLAAIKVMDVTG  
 DEEEEEIKQEINMLKKYSHRNIATYYGAFIKKNPPGMDDQLWLVMFEFCGAGSVTDLIKNT  
 KGNTLKEEWIAYICREILRGLSHLHQHKVIHRDIKQNVLLTENA EVKLVD FGVSAQLDR  
 TVGRNRTFIGTPYWMAPEVIACDENPDATYDFKSDLWSLGITAIEMAEGAPPLCDMHPMR  
 ALFLIPRNPAPRLKSKKWSKKFQSFIESCLVKNHSQRPATEQLMKHPFIRDQPNERQVRI  
 QLKDHIDRTKKKRGEKDETEYEYSGSEEEEEENDSGEPSSILNLPGESTLRRD FLRLQLA  
 NKERSEALRRQOLEQQQRENEEHKRQLLAERQKRIEEQKEQRRRLLEEQQRREKELRKQOE  
 REQRRHYEEQMRREEERRRAEHEQEYIRRLQLEEEQRLLEILQQQLLHEQALLLEYK RKQL  
 EEQQAERLQRQLKQERDYLVS LQHQRQEQRPEVKKPLYHYKEGMS PSEKPAWAKEVEER  
 SRLNRQSSPAMPHKVANRISDPNLPPRSEFSISGVQPARTPPMLRPVDPQIPHVLVAVKS  
 QGPALTASQSVHEQPTKGLSGFQEALNVTSHR VEMPRQNSDPTSENPPLPTRIEKFDRSS  
 WLRQEEDI PPKVPQRTT SISPALARKNSPGNGSALGPRLGSQPIRASNPDLRRTEPILES  
 PLQRTSSGSSSSSTPSSQPSSQGSQPGSQAGSSERTRVRANSKSEGSFVLPHEPAKVK  
 PEESRDITRPSRPASYKKAIDEDLTALAKELRELRIEETNRP MKKVTDYSSSSSEESSE  
 EEEEDGESETHDGTVAVSDI PRLIPTGAPGSNEQYNVGMVGT HGLTSHADSFSGSISRE  
 GTLMIRETSGEKKRSGHSDSNGFAGHINLPDLVQQSHSPAGTPTEGLGRVSTHSQEMDSG  
 TEYGMGSSTKASFTPFVDP RVYQTSPTDEDEDEDESSAALFTSELLRQEQA KLN EARKI  
 SVVNVNPTNIRPHSDTPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSGQGVY  
 NLINRRRFQQMDVLEGLNVLVTTISGKKNKLRVYYLSWLRNRILHNDPEVEKKQGWITVGD  
 LEGCIHYKVVKYERIKFLVIALKNAVEIYAWAPKPYHKFMAFKSFADLQHKPLLVDLTVE  
 EGQRLKVIFGSHTG FHV IDVDSGNSYDIYIPSHIQGNITPHAIVILPKTDGMEMLVCYED  
 EGVYVNTYGRITKDVVLQWGEMPTSVAYIHSNQIMGWGEKAIEIRSVETGHLDG VFMHKKR  
 AQRLKFLCERNDKVFFASVRSGGSSQVFFMTLNRNSMMNW

**FIGURE 6**

## SEQUENCE LISTING

<110> Bird, Timothy A.  
Virca, George Duke  
Martin, Unja  
Anderson, Dirk M.

<120> NOVEL MURINE AND HUMAN KINASES

<130> 2923-WO

<140>

<141>

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 896

<212> DNA

<213> Mus musculus

<400> 1

```

ttggaacgag acgacctgct cggcggcagc ggagtgagcg agccggagcg tgagtggccc 60
cgcggcggcc atgggcgacc cagcccccgc ccgcagcctg gacgacatcg acctgtctgc 120
cctgcgggac cctgcaggaa tctttgagct ggtggagggtg gttggcaatg gaacctatgg 180
acaggtatac aaggggcggc acgtcaagac tgggcagctg gctgccatta aggtcatgga 240
tgtcacagag gatgaggagg aagagatcaa acaggaaatc aacatgttaa agaagtactc 300
tcaccatcgc aatattgcca cctactatgg ggcctttatc aagaagagcc ctccctggga 360
cgatgaccag ctctggctgg tgatggagtt ctgcggtgct ggttcagtga ccgacctggg 420
aaagaacaca aaagggaacg cactgaagga ggattgcatt gcttacatct gcagggagat 480
tctcaggggt cttgcccata tccatgcccc caaggtgatc cacagagata tcaagggaca 540
aaatgtgctg ctgacagaga atgctgaagt caagctagtg gattttgggg tgagtgtcga 600
gctggaccgc actgtgggca ggcggaacac ttctattgga accccatact ggatggctcc 660
agaagtcatt gctgtgacg agaaccctga tgccacctat gactacagga gtgacatttg 720
gtctctagga atcacagcca ttgaaatggc agagggagcc cccctctgtg gtgacatgca 780
ccctatgcgg gccctcttcc tcatccctcg gaaccctccc cccaggctca agtcaaagaa 840
atggtcctaag aagttcactg acttcacatc cacgtgtctc atcaagactt acctga 896

```

<210> 2

<211> 1060

<212> DNA

<213> Mus musculus

<400> 2

```

cggcgcctgc agtggcgcgg ggagaggcga tcggccccgg atccccgcgc cctgcagccc 60
gcgtagaccg agctgccccg gcgccccgaa tcctgaagtc ccagttgagt cagaatggat 120
gaacaatcac aaggaatgca agggccgccc gttactcagt tccagccaca gaaggcatta 180
cggccagata tgggctataa tacttttagc aacttccgaa tagaaaagaa aattggctcg 240
ggacaattta gtgaagttta tagagcatcc tgtctcttgg atggagtgcc ggtagcggtta 300
aaaaaagtac agatatattga tttaatggat gccaaagcac gtgctgattg tatcaaagaa 360
atagacctcc ttaagcaact caaccatcca aatgtaatta aatactatgc atcattcatt 420
gaggataatg agctgaacat agttttggag ttagcagatg ctggtgacct ctccagaatg 480
ataaagcact ttaagaaaca aaagaggcta atccctgaga gaaccgtttg gaaatacttc 540
gttcagctct gcagtgcact ggaccacatg cattctcgaa gagtcatgca cagagatata 600
aaaccagcta atgtgttcat tacagccact ggggtagtaa aactcggaga ccttgggctt 660

```

```

ggtcgggtttt tcagctccaa aaccacagct gcacattctt tagtgggtac accttactac 720
atgtctccag agagaatata tgaaaatgga tacaacttca agtctgacat ctgggtctctt 780
ggctgtctgc tatatgagat ggctgcactg cagagtcctt tctacggcga caagatgaac 840
ttgtattctc tgtgtaagaa gatagagcag tgtgactacc cgctctccc gtcagatcac 900
tattcggagg agctacgaca gctagttaat atatgcatca acccagatcc agagaagcga 960
cccacatcg cctatgttta tgatgtggca aagaggatgc atgcatgtac cgcaagcacc 1020
taaactgtac aagatcctga agcaggctgt ctcgttccaa 1060

```

<210> 3  
 <211> 1694  
 <212> DNA  
 <213> Mus musculus

```

<400> 3
tggaaacgaga cgacctgctc cggagagcag tagaaattag agccagggag ggaccgcggc 60
ggcagcagcc aaggcgaaag aggaaactgc cgaagaggaa gctctgcggc agcccgagcc 120
tccctgcgct ccgcatectc ccgctccgca tcccggcgcc gggcatcccc cggagcccg 180
gccgcgcctc cggcgccctt tcccagcgc aacctcggc cgccctacag cattagtctg 240
ccatggcccc ggagaacggc gagagcagct cctcctggaa aaagcaagca gaagacatta 300
agaagatctt cgagttcaag gagacctcgc gaactggggc cttttctgaa gttgttttag 360
ccgaggagaa agctactggg aagctcttcg cagtgaagtg catcccgaag aaggcgctga 420
agggcaagga gacgagcatc gagaacgaga ttgccgtgct tagaaagatt aagcatgaaa 480
acattgttgc cttggaagat atttatgaaa gcccaaatac cctctacctg gtcattgcaac 540
ttgtgtcttg tggagaactc ttcgatcggc tagtggagaa ggggttttac acagagaaag 600
atgccagcac tctcatccgc caggctcctg atgccgtata ctatctccac agaattgggca 660
ttgtccacag ggacctcaag ccggagaatc tcttatacta cagtcaagac gaggagtcca 720
aaataatgat cagtgaactt ggcttgtcga aaatggaggg caaaggagat gtgatgtcca 780
cggcctgcgg gaccccgagg tatgttgcct cggaagtctt cgcccagaaa ccgtacagca 840
aagctgtgga ctgctgggct atcgggggtg tgcctatat cttgctctgt ggttaccctc 900
ctttttatga tgaaaatgac tcgaagctgt ttgaacagat cctcaaggca gaatatgagt 960
ttgattcccc ctactgggat gacatctccg actctgccaa agacttcatt cggaatctga 1020
tggagaaaaga cccaaataaa agatacactt gtgagcaggg agctcgacac ccatggattg 1080
ctggtgacac agcccttagc aaaaacattc acgaatctgt cagtgccag atccggaaga 1140
attttgcaaa gagcaaatgg agacaagcgt ttaacgccac ggcagtcgtg agacatatgc 1200
ggaggctcca gcttggcagc agcctggaca gttaaatgc aagtgtctca agcaacctca 1260
gtttggccag ccaaaaagat tgtgcgtctg gcaccttcca cgctctgtag tctcctttct 1320
tcttcgtcgg gggctgcagg attcggagct gagaggagac ccaggccac cactgtgaca 1380
acagggcaca ctggaagcaa gtgaccggc tctggagggt gaaccagggg ggcagggccg 1440
gggaaggaga agcccctggc cggagcagct cctgcatcag aaaccacc caccctgcat 1500
ggtgcacctg cataggactg gaagatagaa ggttttttat ggccatattt tatactgcaa 1560
ttctgatgtg ttcatttctc aaaaactgta ctgactgact caaggggagc tggcgtcacg 1620
ggatctgggt ctgtatataa gaatcttgca aagctctaac tgaatggacc ttctagcagg 1680
tcgtctcgtt ccaa 1694

```

<210> 4  
 <211> 2902  
 <212> DNA  
 <213> Mus musculus

```

<400> 4
cactagtgga tccaaagaat tcggcacgag gcgtgctcgg gtgcgggtgt gacctctgag 60
cccgcggctc agcgcgcgct gctactgctg cccgaccac tccacctcgc ggtccccgca 120
ccatggagtc ggtggcctta ctccagcgc cgagccaggc tccctcggcc tccgcccctg 180
cctcggagag cgcggggccg ctggcggacg ggctcatcaa gtcgcctaaa cctctgatga 240
agaagcaggc ggtgaagcgg caccatcaca aacacaacct gcggcaccgc tacgagttcc 300
tggagacgct gggcaagggc acctacggga aggtgaagaa ggcacgagag agctcggggc 360

```

```

gtctgggtggc catcaagtcc atcaggaaaag acaaaatcaa agatgagcag gatctgctgc 420
acatacggag ggagattgag atcatgtctt cactcaacca ccccccacatc attgccatcc 480
atgaagtgtt tgagaatagc agcaagattg tgattgtcat ggagtatgcc agccgaggcg 540
atctgtatga ttacatcagt gagcggccac ggctgagtga gcgggacgcc aggcatttct 600
tccgacagat cgtgtctgcc ctgcactact gccaccagaa cgggatcgtt caccgagatc 660
tcaagctgga aaacatcctt ctgatgcca atggaaacat caagattgct gactttggcc 720
tctccaacct gtaccacaaa ggcaagttcc tccagacgtt ctgtgggagc cctctctacg 780
cctcgccctga gatagtcaac gggaagccct atgtggggccc agaggtggac agctgggtctc 840
tgggcgttct cctgtacatc ctggtgcatg gcaccatgcc ctttgacggg caggatcata 900
aaacactggg gaagcaaadc agtaacgggg cttaccgtga gccgcccagg ccgtccgatg 960
cctgtggcct gatccggtgg ctgttaatgg tgaaccccac ccgtcggggc acactggagg 1020
atgtagccag tcattgggtg gtcaactggg gttacaccac cggagtcggg gaacaggaag 1080
ccctgcgtga ggggtgggcac cctagtgggtg actttggccg ggcctccatg gcggactggt 1140
tacgtcgctc ctcgcgcccc ctctggaga atggagccaa ggtgtgcagc ttcttcaagc 1200
agcaccgacc gggaggtgga agcactgtac ctgggctgga gcggcaacat tctcttaaga 1260
agtcccgaaa ggagaatgac atggctcaaa atctgcaagg tgacccggct gaggatacct 1320
cttctcgccc tggcaagagc agccttaagc ttccgaaagg cattctcaag aaaaagtcct 1380
ctacctcgtc aggggaggta caggaggacc ctacaggaact cagaccggtg cctgatactc 1440
cagggcagcc tgtccctgct gtatccctgc tcccaaggaa aggcacacct aagaagtctc 1500
gacagcgtga atctggttac tactcctctc cagagcccag cgagtctggg gaactcttag 1560
acgccagtga tgtgtttgtg agtggggacc ccgtggagca gaagtctcca caggcttcag 1620
ggctcctcct ccaccgcaag ggcattctca aactcaatgg caagtctctc cgcacagcct 1680
tagaaggcac taccctagc acctttggct ccctggacca actggcctcc tcccatcctg 1740
cagcccgccc cagccgcccc tcaggggctg tgagttagga cagcatcctg tctccgagt 1800
cctttgacca attggacttg cctgaacgtc ttcccgaac cccactgagg ggctgtgtgt 1860
ctgtggacaa cctgaggggg cttgagcagc ctccctcaga aggtctgaag cgatgggtggc 1920
aggaatcctt gggggatagc tgcttttctc tgacagactg ccaagagggtg actgcagcct 1980
acagacaagc cctaggaatc tgctcaaagc tcagctgagg aaggagatg gtgcccctag 2040
atggggtagg ctctgagagg gtttgagag gaaccctggg tcggattcct ccagtgaata 2100
gagtacatca agggctctac gtctgcagcc tgactgaacc tgaaagatga gagaaatcgc 2160
attgatgtgg aaaggaatgg gaacccttgc tgcccagagt ttatagtggg gtggcctgaa 2220
gggtgcctacc tcttttgtgc catgagtgtc acccatgaca tttcccaccc tgttctctgg 2280
ctgcaccttc acataagttt ctgtttccat caaccaccag ggttagaacc ctgacttctc 2340
gggaggtaat gtgtagtga tgccattatt tagagaggaa acagcctctg gtttccatct 2400
ctgctgctgt gcatctcaaa gacctgggaa gactcggacc gctgtttgac ttcactccta 2460
ggggaccaga tgccccctga ccccatctta gatctcagag acttgaacct tgaagctgtt 2520
cctagtaccc agatgtggat ggatgctctg tttctcaggc caacgggacc tagaatgtgc 2580
tgacttattt atttttttgt gattctcact tctgtttttt gggtttttgt tgtttgtttg 2640
ttttttgttt taagtgaatt ttgctgcttt caataatgtg aatgctgtgt tctggggaac 2700
tccactgtgc cactgaagtt tatgtacaga gaagtatttg gcaatgatgt cctctatttc 2760
aaggggggtg ggggcgtttt tcaaattgat gtcttgagca ctgtctggat tgagtctcca 2820
gtcccttcac acccaaggct ggccaccctc cctcatcttc atctgtggcc aaaaaaaaaa 2880
aaaaaaaaaa aaaaaaaaaa aa 2902

```

&lt;210&gt; 5

&lt;211&gt; 3228

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 5

```

tggatccaaa gaattcggca cgaggcggag tccgcctcg ccgcccctcg agcgcccca 60
gcttctctgc tggccggaac ctgcaccccg aaccaggaag cacctggcgg cgggcgcggg 120
atggctgggc ccagctgggg tctccctcgg ctggacgggt tcatccttac cgagcgcctg 180
ggcagtgcca cgtacgccac ggtgtacaag gcctacgcca agaaggatac tcgggaagtg 240
gtagccataa aatgcgtggc caagaagagt ctcaacaagg cgtcagtgga aaacctcctg 300
actgagattg agatcctcaa gggcattcgg caccgccata tcgtgcagct gaaagacttc 360
cagtgggaca atgacaatat ctacctcatc atggagttct gtgcaggggg tgacctgtct 420

```

```

cgcttcattc ataccgcag gatcctgcct gagaagggtgg cccgtgtttt catgcagcag 480
ttggctagtgc cctgcagtt cctgcatgaa cgaaacatct ctcaacttggga tctgaaaccg 540
cagaacatcc tgctgagctc tttggagaag cccacactga aactggcaga ctttggcttt 600
gcccagcaca tgtccccgtg ggacgaaaaa cactgtctcc gtggctcccc gctctatatg 660
gctcctgaga tgggtgtgtcg gcggcagtat gatgcgcgtg tggacctctg gtctgtgggg 720
gtgatcctgt acgaagccct ctttgggcag ccccccttg cctccagatc gttctcagag 780
ctagaagaaa agattcgcag caatcgggtg attgaggtgc gtctggcagg gtctaggcat 840
ccaccgggga ttgagggact caaggccag aagtttgttc agcactgcag tgcaggctct 900
gggcgtttca tggcagtggg gcatgttctg tgggtggaagc cttagtctg gtccgttctc 960
gaggatccat atcagccacg acaggcaaca aatgaccagg cccaatcttc ccatagtccg 1020
gggctggagg caaataccca tttgatagga gactgataaa ggatgcttgg ctctcttctc 1080
gcacatcacc gggacttgcc atgatccact cagattaccc acagcaaaaca cgtaccctta 1140
tgggggttcc taacaggcct tgggctttgg gctcagatgt tggagccttc tgtgatgtgt 1200
ctctgctcta tgcctctgta gctccctctt cggccccaac tctccctaga ctgccgggac 1260
ctgttgacgc gacttctaga gcgggacccc gccgctcgaa tctccttcaa ggacttcttt 1320
gcccacccct ggggtggacct ggagcacatg cccagtgggg agagcctggc acaggcaagg 1380
gcccttgtgg tggaggctgt gaagaaggac caggaggggg atgtgtccgc tgccctgtcg 1440
ctctactgca aggtctctgga cttctttgta cctgcgctac actgtgagaa ccaggccatt 1500
cctataacct gtgtgcagag gggggcagga gttgggtcag gctccccatt cagagcttag 1560
gggagatggg gcagaagatc aacgtggaac tgagtattctg aagattgcaa agggcttact 1620
gtggggtagg ctttcaggac agcatcctca tatgaacct tcaccttctg cagacgaagt 1680
ggatgccag aggaaggagg caattaaggc gaagggtgga cagtattgtt cccgggcaga 1740
ggagctcaaa gccattgtgc cctcctccaa tcaggccctg ctaagacagg gcacaactgt 1800
ccaagagctg cttcgaggct gctccctcac catgagcctt tactctcaca tcagagatgg 1860
cccgtgacaa accacgcctc ctggctgccc tggaaagtggc ctcaagctgcc ctggccaagg 1920
aggaggaagc tggcaaagag caggatgccc tggacctgta ccagcacagc ctcggggagc 1980
tgctagtgtc gttggcagca gaggccccag gccgaaggcg ggagctcctt cacaccgagg 2040
ttcagaacct catggctcga gctgaatacc tgaaggagca gatcaagata agggagtctc 2100
actgggaagc ggagagtctg gacaaagagg ggctgtcgga gtctgttcgt agttcttgca 2160
cactgcagtg acaccggaag gagcagcgga tggagcacia ccctagagag aagctgcatt 2220
accaactcag gttgacacct gcacacctgg gaccttctg gacgagcagc tcccacatgc 2280
tgggtccccag cattcctctg agtgttctcc acccttgggg cgtctggtgg cagggtgtact 2340
aagctctggg agaattactt gaatgtgacc ttgtcattag gtgactgctg gtctaagcct 2400
gtccggcttc aggacacct caccocgttg tgttttgttc tgcaaagagg acgtcatgcc 2460
tcttcaggac acttgctacc agacagctgc tgtacctggg ccacccctcc ctgggagcct 2520
ttattccaac cctacttttt ttcttgcact ggaatgggac actcggatac cctcagggac 2580
tacctacctg acagtatgct ctgggtcttc agacctctcc agtcttcttg atgaaagtca tgcccttgt 2700
gctgccatcc ttttcagttc tttaagacaa tcttctcatgc atgaaagtca tgcccttgt 2760
aaagggtgaa tacatgtgag aaccccagac ctctcctgcc cactagtcac atgggtggacc 2820
tcataccccc acttacagct ctctttgagg ggatattgcca cctattaagc tatggataca 2880
ctgagctaga gctgggtctt ggctgggtct tccccctgtt aagaacttac gtatctggag ttactggaag 2940
tccacagctt ataccctgta tgagctggag aagaacttac cccctcccc caggteatca tcttgtttca 3000
attgctcttt ttttttttct tctttaaaca cccctcccc aaggagcaga ggagctgttc 3060
gattttttatt caaattctta ttgaaggctg atttttgaat tttcttctct ccttcttctc 3120
tgccacaaat gacccccaaa tgacaggcac tgagactttc tttcttctct tcttcttctc 3180
ttccttctct ccttcttctc tcttcttctc tcttcttctc tcttcttctc 3228

```

&lt;210&gt; 6

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

```

cgcatgagga cgcgagtga atagaccaag gtggaatttc caagggaata gcttcggggg 60
ggttttgggtc cttttctcca gcgaagaagt agacatggcg agcgactccc cggctcgaag 120
cctggatgaa atagatctct cggctctgag ggaccctgca gggatctttg aattgggtgga 180

```



```

acttggttga aatggaacat acgggcaagt ttataagggg cgtcatgtca aaacggggcca 240
gcttgcagcc atcaagggtta tggatgtcac aggggatgaa gaggaagaaa tcaaacaaga 300
aattaacatg ttgaagaaat attctcatca ccggaatatt gctacatact atggtgcttt 360
tatcaaaaag aacccaccag gcatggatga ccaactttgg ttggtgatgg agttttgtgg 420
tgctggctct gtcaccgacc tgatcaagaa cacaaaaggt aacacgttga aagaggagtg 480
gattgcatac atctgcaggg aaatcttacg ggggtgagt cacctgcacc agcataaagt 540
gattcatcga gatattaaag ggcaaaatgt cttgctgact gaaaatgcag aagttaaact 600
agtggacttt ggagtcagtg ctcagcttga tcgaacagtg ggcaggagga atactttcat 660
tggaactccc tactggatgg caccagaagt tattgcctgt gatgaaaacc cagatgccac 720
atatgatttc aagagtgact tgtggtcttt ggggtatcac gccattgaaa tggcagaagg 780
tgctccccct ctctgtgaca tgcaccccat gagagctctc ttctcatcc cccggaatcc 840
agcgctcgg ctgaagtcta agaagtggc aaaaaaatt ccagtcattt attgagagct 900
gcttggtaaa gaatcacagc cagcgaccag caacagaaca attgatgaag catccattta 960
tacgagacca acctaatgag cgacagggtc gcattcaact caaggaccat attgatagaa 1020
caaagaagaa gcgag 1035

```

&lt;210&gt; 7

&lt;211&gt; 4083

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

```

atggcgagcg actccccggc tcgaagcctg gatgaaatag atctctcggc tctgagggac 60
cctgcaggga tctttgaatt ggtggaactt gttggaaatg gaacatacgg gcaagtttat 120
aagggtcgtc atgtcaaaac gggccagctt gcagccatca aggttatgga tgtcacaggg 180
gatgaagagg aagaaatcaa acaagaaatt aacatgttga agaaatattc tcatcaccgg 240
aatattgcta catactatgg tgcttttacc aaaaagaacc caccaggcat ggatgaccaa 300
ctttggttgg tgatggagtt ttgtggtgct ggctctgtca ccgacctgat caagaacaca 360
aaaggtaaca cgttgaaaga ggagtggatt gcatacatct gcagggaaat cttacggggg 420
ctgagtcacc tgcaccagca taaagtgatt catcgagata ttaaagggca aaatgtcttg 480
ctgactgaaa atgcagaagt taaactagtg gactttggag tcagtgtctca gcttgatcga 540
acagtgggca ggaggaatac ttctatttga actccctact ggatggcacc agaagttatt 600
gcctgtgatg aaaaccacga tgccacatat gatttcaaga gtgacttggt gtctttgggt 660
atcacggcca ttgaaatggc agaagggtct cccctctct gtgacatgca ccccatgaga 720
gctctcttcc tcatcccccg gaatccagcg cctcggctga agtctaagaa gtgggtcaaaa 780
aaattccagt catttattga gagctgcttg gtaagaatc acagccagcg accagcaaca 840
gaacaattga tgaagcatcc atttatacga gaccaaccta atgagcgaca ggtccgcatt 900
caactcaagg accatattga tagaacaag aagaagcgag gagaaaaaga tgagacagag 960
tatgagtaca gtggaagtga ggaagaagag gaggagaatg actcaggaga gccagctcc 1020
atcctgaatc tgccagggga gtcgacgctg cggagggact ttctgaggct gcagctggcc 1080
aacaaggagc gttctgaggc cctacggagg cagcagctgg agcagcagca gcgggagaa 1140
gaggagcaca agcggcagct gctggccgag cgctcagaagc gcatcgagga gcagaaagag 1200
cagaggcggc ggctggaggga gcaacaaagg cgagagaagg agctgcggaa gcagcaggag 1260
agggagcagc gccggcacta tgaggagcag atgcgccggg agggaggagag gaggcgctcg 1320
gagcatgaac aggaatacat caggcgacag ttagaggagg agcagagaca gttagagatc 1380
ttgcagcagc agctactgca tgaacaagct ctacttcttg aatataagcg caaacaattg 1440
gaagaacaga gacaagcaga aagactgcag aggcagctaa agcaagaaag agactactta 1500
gtttcccttc agcatcagcg gcaggagcag aggcctgttg agaagaagcc actgtaccat 1560
tacaagaag gaatgagtc tagtgagaag ccagcatggg ccaaggaggt agaagaacgg 1620
tcaaggctca accggcaaag ttcccttgcc atgcctcaca aggttgccaa caggatatct 1680
gaccccaacc tgcccccaag gtccggagtcc ttcagcatta gtggagttca gcctgctcga 1740
acacccccca tgctcagacc agtcgatccc cagatcccac atctggtagc tgtaaaatcc 1800
cagggacctg ccttgaccgc ctcccagtc gtgcacgagc agcccacaaa gggcctctct 1860
gggtttcagg aggtctctgaa cgtgacctcc caccgcgttg agatgccacg ccagaactca 1920
gateccacct cggaaaatcc tctctctccc actcgcattg aaaagtttga ccgaagctct 1980
tggttacgac aggaagaaga cattccacca aaggtgcctc aaagaacaac ttctatatcc 2040
ccagcattag ccagaagaa ttctcctggg aatggtagtg ctctgggacc cagactagga 2100

```

```

tctcaaccca tcagagcaag caaccctgat ctccggagaa ctgagcccat cttgggagagc 2160
cccttgacaga ggaccagcag tggcagttcc tccagctcca gcacccttag ctcccagccc 2220
agctcccaag gaggtctcca gcctggatca caagcaggat ccagtgaacg caccagagtt 2280
cgagccaaca gtaagtcaga aggatcacct gtgcttcccc atgagcctgc caaggtgaaa 2340
ccagaagaat ccagggacat taccggccc agtcgaccag ctagctacaa aaaagctata 2400
gatgaggatc tgacggcatt agccaaagaa ctaagagaac tccggattga agaaacaaac 2460
cgcccaatga agaagggtgac tgattactcc tcttccagtg aggagtcaga aagtagcgag 2520
gaagaggagg aagatggaga gagcgagacc catgatggga cagtggctgt cagcgacata 2580
cccagactga taccaacagg agctccaggc agcaacgagc agtacaatgt gggaatgggtg 2640
gggacgcatg ggctggagac ctctcatgcg gacagtttca gcggcagtat ttcaagagaa 2700
ggaaccttga tgattagaga gacgtctgga gagaagaagc gatctggcca cagtgcagac 2760
aatggctttg ctggccacat caacctccct gacctgggtg agcagagcca ttctccagct 2820
ggaacccga ctgagggact ggggcgcgtc tcaacccatt cccaggagat ggactctggg 2880
actgaatatg gcatggggag cagcaccaaa gcctccttca cccctttgtt ggacccaga 2940
gtataccaga cgtctccac tgatgaagat gaagaggatg aggaatcatc agccgcagct 3000
ctgtttacta gcgaacttct taggcaagaa caggccaaac tcaatgaagc aagaaagatt 3060
tcgggtggtaa atgtaaaccc aaccaacatt cggcctcata gcgacacacc agaaatcaga 3120
aaatacaaga aacgattcaa ctacagaaata ctttgtgcag ctctgtgggg tgtaaaccctt 3180
ctgggtgggga ctgaaaatgg cctgatgctt ttggaccgaa gtgggcaagg caaagtctat 3240
aatctgatca accggaggcg atttcagcag atggatgtgc tagagggact gaatgtcctt 3300
gtgacaattt caggaaagaa gaataagcta cgagtttact atctttcatg gttaagaaaac 3360
agaatactac ataatgaccc agaagtagaa aagaaacaag gctggatcac tgttggggac 3420
ttggaaggct gtatacatga taaagttgtt aaatatgaaa ggatcaaatt tttggtgatt 3480
gccttaaaga atgctgtgga aatatatgct tgggctccta aaccgtatca taaattcatg 3540
gcatttaagt cttttgcaga tctccagcac aagcctctgc tcacacactg gtttccatgt aattgatgtt 3600
gaagggtcaaa gattaaaggt tatttttgggt tatctacata ccattctcata ttcaggggcaa tatcactcct 3720
gattcaggaa actcttatga tatctacata ccattctcata ttcaggggcaa tatcactcct 3780
catgctattg tcatcttgcc taaaacagat ggaatggaaa tgcttgtttg ctatgaggat 3840
gagggggtgt atgtaaacac ctatggccgg ataactaagg atgtggtgct ccaatgggga 3900
gaaatgccc cgtctgtggc ctacattcat tccaatcaga taatgggctg gggcgagaaa 3960
gctattgaga tccggtcagt ggaaacagga catttgatg gagtatttat gcataagcga 3960
gctcaaaggt taaagtttct atgtgaaaga aatgataagg tattttttgc atccgtgcga 4020
tctggaggaa gtagccaagt gtttttcatg accctcaaca gaaattccat gatgaactgg 4080
taa

```

<210> 8  
 <211> 275  
 <212> PRT  
 <213> Mus musculus

<400> 8  
 Met Gly Asp Pro Ala Pro Ala Arg Ser Leu Asp Asp Ile Asp Leu Ser  
 1 5 10 15  
 Ala Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Val Val Gly  
 20 25 30  
 Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Gly  
 35 40 45  
 Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu Glu  
 50 55 60  
 Glu Ile Lys Gln Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg  
 65 70 75 80

Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Ser Pro Pro Gly  
                                     85                                    90                                    95  
 Asn Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser  
                                     100                                    105                                    110  
 Val Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Ala Leu Lys Glu Asp  
                                     115                                    120                                    125  
 Cys Ile Ala Tyr Ile Cys Arg Glu Ile Leu Arg Gly Leu Ala His Leu  
                                     130                                    135                                    140  
 His Ala His Lys Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu  
                                     145                                    150                                    155                                    160  
 Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala  
                                     165                                    170                                    175  
 Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro  
                                     180                                    185                                    190  
 Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala  
                                     195                                    200                                    205  
 Thr Tyr Asp Tyr Arg Ser Asp Ile Trp Ser Leu Gly Ile Thr Ala Ile  
                                     210                                    215                                    220  
 Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg  
                                     225                                    230                                    235                                    240  
 Ala Leu Phe Leu Ile Pro Arg Asn Pro Pro Pro Arg Leu Lys Ser Lys  
                                     245                                    250                                    255  
 Lys Trp Ser Lys Lys Phe Thr Asp Phe Ile Asp Thr Cys Leu Ile Lys  
                                     260                                    265                                    270  
 Thr Tyr Leu  
                                     275

<210> 9  
 <211> 302  
 <212> PRT  
 <213> Mus musculus

<400> 9  
 Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Thr Gln Phe  
                                     1                                    5                                    10                                    15  
 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala  
                                     20                                    25                                    30  
 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val  
                                     35                                    40                                    45  
 Tyr Arg Ala Ser Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys  
                                     50                                    55                                    60

Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile  
 65 70 75 80  
 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys  
 85 90 95  
 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu  
 100 105 110  
 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys  
 115 120 125  
 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln  
 130 135 140  
 Leu Cys Ser Ala Leu Asp His Met His Ser Arg Arg Val Met His Arg  
 145 150 155 160  
 Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys  
 165 170 175  
 Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala  
 180 185 190  
 Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile  
 195 200 205  
 His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys  
 210 215 220  
 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys  
 225 230 235 240  
 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro  
 245 250 255  
 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn  
 260 265 270  
 Ile Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val  
 275 280 285  
 Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr  
 290 295 300  
  
 <210> 10  
 <211> 355  
 <212> PRT  
 <213> Mus musculus  
  
 <400> 10  
 Met Ala Arg Glu Asn Gly Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala  
 1 5 10 15  
 Glu Asp Ile Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly  
 20 25 30

Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu  
                   35                                  40                                  45  
 Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser  
           50                                  55                                  60  
 Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn  
       65                                  70                                  75                                  80  
 Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu  
                                   85                                  90                                  95  
 Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu  
                                   100                                  105                                  110  
 Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val  
           115                                  120                                  125  
 Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp  
       130                                  135                                  140  
 Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys  
       145                                  150                                  155                                  160  
 Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp  
                                   165                                  170                                  175  
 Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val  
                                   180                                  185                                  190  
 Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly  
           195                                  200                                  205  
 Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu  
       210                                  215                                  220  
 Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe  
       225                                  230                                  235                                  240  
 Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile  
                                   245                                  250                                  255  
 Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln  
           260                                  265                                  270  
 Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Ser Lys Asn  
           275                                  280                                  285  
 Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser  
       290                                  295                                  300  
 Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg  
       305                                  310                                  315                                  320  
 Arg Leu Gln Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser  
                                   325                                  330                                  335

Ser Asn Leu Ser Leu Ala Ser Gln Lys Asp Cys Ala Ser Gly Thr Phe  
 340 345 350

His Ala Leu  
 355

<210> 11  
 <211> 631  
 <212> PRT  
 <213> Mus musculus

<400> 11  
 Met Glu Ser Val Ala Leu Leu Gln Arg Pro Ser Gln Ala Pro Ser Ala  
 1 5 10 15  
 Ser Ala Leu Ala Ser Glu Ser Ala Arg Pro Leu Ala Asp Gly Leu Ile  
 20 25 30  
 Lys Ser Pro Lys Pro Leu Met Lys Lys Gln Ala Val Lys Arg His His  
 35 40 45  
 His Lys His Asn Leu Arg His Arg Tyr Glu Phe Leu Glu Thr Leu Gly  
 50 55 60  
 Lys Gly Thr Tyr Gly Lys Val Lys Lys Ala Arg Glu Ser Ser Gly Arg  
 65 70 75 80  
 Leu Val Ala Ile Lys Ser Ile Arg Lys Asp Lys Ile Lys Asp Glu Gln  
 85 90 95  
 Asp Leu Leu His Ile Arg Arg Glu Ile Glu Ile Met Ser Ser Leu Asn  
 100 105 110  
 His Pro His Ile Ile Ala Ile His Glu Val Phe Glu Asn Ser Ser Lys  
 115 120 125  
 Ile Val Ile Val Met Glu Tyr Ala Ser Arg Gly Asp Leu Tyr Asp Tyr  
 130 135 140  
 Ile Ser Glu Arg Pro Arg Leu Ser Glu Arg Asp Ala Arg His Phe Phe  
 145 150 155 160  
 Arg Gln Ile Val Ser Ala Leu His Tyr Cys His Gln Asn Gly Ile Val  
 165 170 175  
 His Arg Asp Leu Lys Leu Glu Asn Ile Leu Leu Asp Ala Asn Gly Asn  
 180 185 190  
 Ile Lys Ile Ala Asp Phe Gly Leu Ser Asn Leu Tyr His Lys Gly Lys  
 195 200 205  
 Phe Leu Gln Thr Phe Cys Gly Ser Pro Leu Tyr Ala Ser Pro Glu Ile  
 210 215 220  
 Val Asn Gly Lys Pro Tyr Val Gly Pro Glu Val Asp Ser Trp Ser Leu  
 225 230 235 240

Gly Val Leu Leu Tyr Ile Leu Val His Gly Thr Met Pro Phe Asp Gly  
 245 250 255  
 Gln Asp His Lys Thr Leu Val Lys Gln Ile Ser Asn Gly Ala Tyr Arg  
 260 265 270  
 Glu Pro Pro Lys Pro Ser Asp Ala Cys Gly Leu Ile Arg Trp Leu Leu  
 275 280 285  
 Met Val Asn Pro Thr Arg Arg Ala Thr Leu Glu Asp Val Ala Ser His  
 290 295 300  
 Trp Trp Val Asn Trp Gly Tyr Thr Thr Gly Val Gly Glu Gln Glu Ala  
 305 310 315 320  
 Leu Arg Glu Gly Gly His Pro Ser Gly Asp Phe Gly Arg Ala Ser Met  
 325 330 335  
 Ala Asp Trp Leu Arg Arg Ser Ser Arg Pro Leu Leu Glu Asn Gly Ala  
 340 345 350  
 Lys Val Cys Ser Phe Phe Lys Gln His Val Pro Gly Gly Gly Ser Thr  
 355 360 365  
 Val Pro Gly Leu Glu Arg Gln His Ser Leu Lys Lys Ser Arg Lys Glu  
 370 375 380  
 Asn Asp Met Ala Gln Asn Leu Gln Gly Asp Pro Ala Glu Asp Thr Ser  
 385 390 395 400  
 Ser Arg Pro Gly Lys Ser Ser Leu Lys Leu Pro Lys Gly Ile Leu Lys  
 405 410 415  
 Lys Lys Ser Ser Thr Ser Ser Gly Glu Val Gln Glu Asp Pro Gln Glu  
 420 425 430  
 Leu Arg Pro Val Pro Asp Thr Pro Gly Gln Pro Val Pro Ala Val Ser  
 435 440 445  
 Leu Leu Pro Arg Lys Gly Ile Leu Lys Lys Ser Arg Gln Arg Glu Ser  
 450 455 460  
 Gly Tyr Tyr Ser Ser Pro Glu Pro Ser Glu Ser Gly Glu Leu Leu Asp  
 465 470 475 480  
 Ala Ser Asp Val Phe Val Ser Gly Asp Pro Val Glu Gln Lys Ser Pro  
 485 490 495  
 Gln Ala Ser Gly Leu Leu Leu His Arg Lys Gly Ile Leu Lys Leu Asn  
 500 505 510  
 Gly Lys Phe Ser Arg Thr Ala Leu Glu Gly Thr Thr Pro Ser Thr Phe  
 515 520 525  
 Gly Ser Leu Asp Gln Leu Ala Ser Ser His Pro Ala Ala Arg Pro Ser  
 530 535 540

Arg Pro Ser Gly Ala Val Ser Glu Asp Ser Ile Leu Ser Ser Glu Ser  
545 550 555 560

Phe Asp Gln Leu Asp Leu Pro Glu Arg Leu Pro Glu Thr Pro Leu Arg  
565 570 575

Gly Cys Val Ser Val Asp Asn Leu Arg Gly Leu Glu Gln Pro Pro Ser  
580 585 590

Glu Gly Leu Lys Arg Trp Trp Gln Glu Ser Leu Gly Asp Ser Cys Phe  
595 600 605

Ser Leu Thr Asp Cys Gln Glu Val Thr Ala Ala Tyr Arg Gln Ala Leu  
610 615 620

Gly Ile Cys Ser Lys Leu Ser  
625 630

<210> 12

<211> 311

<212> PRT

<213> Mus musculus

<400> 12

Met Ala Gly Pro Ser Trp Gly Leu Pro Arg Leu Asp Gly Phe Ile Leu  
1 5 10 15

Thr Glu Arg Leu Gly Ser Gly Thr Tyr Ala Thr Val Tyr Lys Ala Tyr  
20 25 30

Ala Lys Lys Asp Thr Arg Glu Val Val Ala Ile Lys Cys Val Ala Lys  
35 40 45

Lys Ser Leu Asn Lys Ala Ser Val Glu Asn Leu Leu Thr Glu Ile Glu  
50 55 60

Ile Leu Lys Gly Ile Arg His Pro His Ile Val Gln Leu Lys Asp Phe  
65 70 75 80

Gln Trp Asp Asn Asp Asn Ile Tyr Leu Ile Met Glu Phe Cys Ala Gly  
85 90 95

Gly Asp Leu Ser Arg Phe Ile His Thr Arg Arg Ile Leu Pro Glu Lys  
100 105 110

Val Ala Arg Val Phe Met Gln Gln Leu Ala Ser Ala Leu Gln Phe Leu  
115 120 125

His Glu Arg Asn Ile Ser His Leu Asp Leu Lys Pro Gln Asn Ile Leu  
130 135 140

Leu Ser Ser Leu Glu Lys Pro His Leu Lys Leu Ala Asp Phe Gly Phe  
145 150 155 160

Ala Gln His Met Ser Pro Trp Asp Glu Lys His Val Leu Arg Gly Ser  
165 170 175



Pro Leu Tyr Met Ala Pro Glu Met Val Cys Arg Arg Gln Tyr Asp Ala  
 180 185 190

Arg Val Asp Leu Trp Ser Val Gly Val Ile Leu Tyr Glu Ala Leu Phe  
 195 200 205

Gly Gln Pro Pro Phe Ala Ser Arg Ser Phe Ser Glu Leu Glu Glu Lys  
 210 215 220

Ile Arg Ser Asn Arg Val Ile Glu Val Arg Leu Ala Gly Ser Arg His  
 225 230 235 240

Pro Pro Gly Ile Glu Gly Leu Lys Ala Gln Lys Phe Val Gln His Cys  
 245 250 255

Ser Ala Gly Ser Gly Arg Phe Met Ala Val Gly His Val Leu Trp Trp  
 260 265 270

Lys Pro Arg Val Trp Ser Val Pro Glu Asp Pro Tyr Gln Pro Arg Gln  
 275 280 285

Ala Thr Asn Asp Gln Ala Gln Ser Ser His Ser Pro Gly Leu Glu Ala  
 290 295 300

Asn Thr His Leu Ile Gly Asp  
 305 310

<210> 13  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 13  
 Met Ala Ser Asp Ser Pro Ala Arg Ser Leu Asp Glu Ile Asp Leu Ser  
 1 5 10 15

Ala Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Leu Val Gly  
 20 25 30

Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Gly  
 35 40 45

Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Gly Asp Glu Glu Glu  
 50 55 60

Glu Ile Lys Gln Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg  
 65 70 75 80

Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Asn Pro Pro Gly  
 85 90 95

Met Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser  
 100 105 110

Val Thr Asp Leu Ile Lys Asn Thr Lys Gly Asn Thr Leu Lys Glu Glu  
 115 120 125

Trp Ile Ala Tyr Ile Cys Arg Glu Ile Leu Arg Gly Leu Ser His Leu  
 130 135 140  
 His Gln His Lys Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu  
 145 150 155 160  
 Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala  
 165 170 175  
 Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro  
 180 185 190  
 Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala  
 195 200 205  
 Thr Tyr Asp Phe Lys Ser Asp Leu Trp Ser Leu Gly Ile Thr Ala Ile  
 210 215 220  
 Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg  
 225 230 235 240  
 Ala Leu Phe Leu Ile Pro Arg Asn Pro Ala Pro Arg Leu Lys Ser Lys  
 245 250 255  
 Lys Trp Ser Lys Lys Ile Pro Val Ile Tyr  
 260 265

<210> 14  
 <211> 1360  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Met Ala Ser Asp Ser Pro Ala Arg Ser Leu Asp Glu Ile Asp Leu Ser  
 1 5 10 15  
 Ala Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Leu Val Gly  
 20 25 30  
 Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Gly  
 35 40 45  
 Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Gly Asp Glu Glu Glu  
 50 55 60  
 Glu Ile Lys Gln Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg  
 65 70 75 80  
 Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Asn Pro Pro Gly  
 85 90 95  
 Met Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser  
 100 105 110  
 Val Thr Asp Leu Ile Lys Asn Thr Lys Gly Asn Thr Leu Lys Glu Glu  
 115 120 125

Trp Ile Ala Tyr Ile Cys Arg Glu Ile Leu Arg Gly Leu Ser His Leu  
 130 135 140  
 His Gln His Lys Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu  
 145 150 155 160  
 Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala  
 165 170 175  
 Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro  
 180 185 190  
 Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala  
 195 200 205  
 Thr Tyr Asp Phe Lys Ser Asp Leu Trp Ser Leu Gly Ile Thr Ala Ile  
 210 215 220  
 Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg  
 225 230 235 240  
 Ala Leu Phe Leu Ile Pro Arg Asn Pro Ala Pro Arg Leu Lys Ser Lys  
 245 250 255  
 Lys Trp Ser Lys Lys Phe Gln Ser Phe Ile Glu Ser Cys Leu Val Lys  
 260 265 270  
 Asn His Ser Gln Arg Pro Ala Thr Glu Gln Leu Met Lys His Pro Phe  
 275 280 285  
 Ile Arg Asp Gln Pro Asn Glu Arg Gln Val Arg Ile Gln Leu Lys Asp  
 290 295 300  
 His Ile Asp Arg Thr Lys Lys Lys Arg Gly Glu Lys Asp Glu Thr Glu  
 305 310 315 320  
 Tyr Glu Tyr Ser Gly Ser Glu Glu Glu Glu Glu Glu Asn Asp Ser Gly  
 325 330 335  
 Glu Pro Ser Ser Ile Leu Asn Leu Pro Gly Glu Ser Thr Leu Arg Arg  
 340 345 350  
 Asp Phe Leu Arg Leu Gln Leu Ala Asn Lys Glu Arg Ser Glu Ala Leu  
 355 360 365  
 Arg Arg Gln Gln Leu Glu Gln Gln Gln Arg Glu Asn Glu Glu His Lys  
 370 375 380  
 Arg Gln Leu Leu Ala Glu Arg Gln Lys Arg Ile Glu Glu Gln Lys Glu  
 385 390 395 400  
 Gln Arg Arg Arg Leu Glu Glu Gln Gln Arg Arg Glu Lys Glu Leu Arg  
 405 410 415  
 Lys Gln Gln Glu Arg Glu Gln Arg Arg His Tyr Glu Glu Gln Met Arg  
 420 425 430

Arg Glu Glu Glu Arg Arg Arg Ala Glu His Glu Gln Glu Tyr Ile Arg  
 435 440 445  
 Arg Gln Leu Glu Glu Glu Gln Arg Gln Leu Glu Ile Leu Gln Gln Gln  
 450 455 460  
 Leu Leu His Glu Gln Ala Leu Leu Leu Glu Tyr Lys Arg Lys Gln Leu  
 465 470 475 480  
 Glu Glu Gln Arg Gln Ala Glu Arg Leu Gln Arg Gln Leu Lys Gln Glu  
 485 490 495  
 Arg Asp Tyr Leu Val Ser Leu Gln His Gln Arg Gln Glu Gln Arg Pro  
 500 505 510  
 Val Glu Lys Lys Pro Leu Tyr His Tyr Lys Glu Gly Met Ser Pro Ser  
 515 520 525  
 Glu Lys Pro Ala Trp Ala Lys Glu Val Glu Glu Arg Ser Arg Leu Asn  
 530 535 540  
 Arg Gln Ser Ser Pro Ala Met Pro His Lys Val Ala Asn Arg Ile Ser  
 545 550 555 560  
 Asp Pro Asn Leu Pro Pro Arg Ser Glu Ser Phe Ser Ile Ser Gly Val  
 565 570 575  
 Gln Pro Ala Arg Thr Pro Pro Met Leu Arg Pro Val Asp Pro Gln Ile  
 580 585 590  
 Pro His Leu Val Ala Val Lys Ser Gln Gly Pro Ala Leu Thr Ala Ser  
 595 600 605  
 Gln Ser Val His Glu Gln Pro Thr Lys Gly Leu Ser Gly Phe Gln Glu  
 610 615 620  
 Ala Leu Asn Val Thr Ser His Arg Val Glu Met Pro Arg Gln Asn Ser  
 625 630 635 640  
 Asp Pro Thr Ser Glu Asn Pro Pro Leu Pro Thr Arg Ile Glu Lys Phe  
 645 650 655  
 Asp Arg Ser Ser Trp Leu Arg Gln Glu Glu Asp Ile Pro Pro Lys Val  
 660 665 670  
 Pro Gln Arg Thr Thr Ser Ile Ser Pro Ala Leu Ala Arg Lys Asn Ser  
 675 680 685  
 Pro Gly Asn Gly Ser Ala Leu Gly Pro Arg Leu Gly Ser Gln Pro Ile  
 690 695 700  
 Arg Ala Ser Asn Pro Asp Leu Arg Arg Thr Glu Pro Ile Leu Glu Ser  
 705 710 715 720  
 Pro Leu Gln Arg Thr Ser Ser Gly Ser Ser Ser Ser Ser Thr Pro  
 725 730 735

Ser Ser Gln Pro Ser Ser Gln Gly Gly Ser Gln Pro Gly Ser Gln Ala  
 740 745 750  
 Gly Ser Ser Glu Arg Thr Arg Val Arg Ala Asn Ser Lys Ser Glu Gly  
 755 760 765  
 Ser Pro Val Leu Pro His Glu Pro Ala Lys Val Lys Pro Glu Glu Ser  
 770 775 780  
 Arg Asp Ile Thr Arg Pro Ser Arg Pro Ala Ser Tyr Lys Lys Ala Ile  
 785 790 795 800  
 Asp Glu Asp Leu Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile  
 805 810 815  
 Glu Glu Thr Asn Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser  
 820 825 830  
 Ser Glu Glu Ser Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser  
 835 840 845  
 Glu Thr His Asp Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile  
 850 855 860  
 Pro Thr Gly Ala Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val  
 865 870 875 880  
 Gly Thr His Gly Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser  
 885 890 895  
 Ile Ser Arg Glu Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys  
 900 905 910  
 Lys Arg Ser Gly His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn  
 915 920 925  
 Leu Pro Asp Leu Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr  
 930 935 940  
 Glu Gly Leu Gly Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly  
 945 950 955 960  
 Thr Glu Tyr Gly Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe  
 965 970 975  
 Val Asp Pro Arg Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu  
 980 985 990  
 Asp Glu Glu Ser Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg  
 995 1000 1005  
 Gln Glu Gln Ala Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn  
 1010 1015 1020  
 Val Asn Pro Thr Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg  
 1025 1030 1035 1040

Lys Tyr Lys Lys Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp  
 1045 1050 1055  
 Gly Val Asn Leu Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp  
 1060 1065 1070  
 Arg Ser Gly Gln Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe  
 1075 1080 1085  
 Gln Gln Met Asp Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser  
 1090 1095 1100  
 Gly Lys Lys Asn Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn  
 1105 1110 1115 1120  
 Arg Ile Leu His Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile  
 1125 1130 1135  
 Thr Val Gly Asp Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr  
 1140 1145 1150  
 Glu Arg Ile Lys Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile  
 1155 1160 1165  
 Tyr Ala Trp Ala Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser  
 1170 1175 1180  
 Phe Ala Asp Leu Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu  
 1185 1190 1195 1200  
 Glu Gly Gln Arg Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His  
 1205 1210 1215  
 Val Ile Asp Val Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser  
 1220 1225 1230  
 His Ile Gln Gly Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys  
 1235 1240 1245  
 Thr Asp Gly Met Glu Met Leu Val Cys Tyr Glu Asp Glu Gly Val Tyr  
 1250 1255 1260  
 Val Asn Thr Tyr Gly Arg Ile Thr Lys Asp Val Val Leu Gln Trp Gly  
 1265 1270 1275 1280  
 Glu Met Pro Thr Ser Val Ala Tyr Ile His Ser Asn Gln Ile Met Gly  
 1285 1290 1295  
 Trp Gly Glu Lys Ala Ile Glu Ile Arg Ser Val Glu Thr Gly His Leu  
 1300 1305 1310  
 Asp Gly Val Phe Met His Lys Arg Ala Gln Arg Leu Lys Phe Leu Cys  
 1315 1320 1325  
 Glu Arg Asn Asp Lys Val Phe Phe Ala Ser Val Arg Ser Gly Gly Ser  
 1330 1335 1340

Ser Gln Val Phe Phe Met Thr Leu Asn Arg Asn Ser Met Met Asn Trp  
1345 1350 1355 1360

<210> 15

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide  
primer

<400> 15

atggcgagcg actccccggc tcgaa

25

<210> 16

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide  
primer

<400> 16

ccagttcatc atggaatttc tggtgaggg

29 ,

1

3

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/14696

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : Please See Extra Sheet.

US CL : 536/23.1, 23.2, 435/194, 320.1, 252.3, 325, 15; 530/387.9

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 23.2, 435/194, 320.1, 252.3, 325, 15; 530/387.9

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P ----- Y,P	Database GenBank, on STN. US National Library of Medicine (Bethesda MD), No. AB035697. Watanabe et al. 'Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development'. FEBS Lett. 469 (1), 19-23, April 2000.	1-3, 7, 10 ----- 4-6, 8-9, 11-16
X,P ----- Y,P	Database GenBank on STN. US National Library of Medicine (Bethesda MD), No. AB041925. Watanabe et al. 'Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development. FEBS Lett. 469 (1) 19-23, April 2000.	1-3, 7, 10 ----- 4-6, 8-9, 11-16

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*B* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G* document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

13 SEPTEMBER 2000

Date of mailing of the international search report

04 OCT 2000

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

REBECCA PROUTY

Telephone No. (703) 308-0196



## INTERNATIONAL SEARCH REPORT

 International application No.  
 PCT/US00/14696

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ---- Y	SU, Y. et al. NIK is a New Ste20-Related Kinase That Binds NCK and MEKK1 and Activates the SAPK/JNK Cascade Via a Conserved Regulatory Domain. EMBO J. 1997, Vol. 16, No. 6, pages 1279-1290. see entire document.	1-3, 5, 7-10 ----- 4, 6, 11-16
X --- Y	YAO, Z. et al. A Novel Human STE20-Related Protein Kinase, HGK, That Specifically Activates the c-Jun N-Terminal Kinase Signaling Pathway. J. Biol. Chem. 22 January 1999, Vol. 274 No. 4, pages 2118-2125, see entire document.	1-3, 5, 7-10 ----- 4, 6, 11-16
X,P ----- Y,P	Database GenBank on STN. US National Library of Medicine (Bethesda MD), No. AB026289. Saito et al. "Direct Submission". October 1999.	1-3, 7, 10 ----- 4-6, 8-9, 11-16
X --- Y	Database GenBank on STN. US National Library of Medicine (Bethesda MD), No. AI469033. March 1999	1-2, 7 ----- 3-6, 8-16
X --- Y	PICCIOTTO, M.R. et al. Calcium/Calmodulin-Dependent Protein Kinase I. J. Biol. Chem. 15 December 1993, Vol. 268, No. 35, pages 26512-26521. see entire document.	1-4, 7-10 ----- 5, 6, 11-16
X --- Y	Database GenBank on STN. US National Library of Medicine (Bethesda MD), No. AA018361. NCI-CGAP, July 1996.	1-2, 7 ----- 3-6, 8-16
X --- Y	Database GenBank on STN. US National Library of Medicine (Bethesda MD), No. AB011123, Ohara et al. "Direct Submission". April 1998.	1, 2, 7 ----- 3-6, 8-16
X,P ----- Y,P	FU, C.A. et al., TNIK, A Novel Member of the Germinal Center Kinase Family That Activates the c-Jun N-Terminal Kinase Pathway and Regulates the Cytoskeleton. J. Biol. Chem. October 1999, Vol. 274, No. 43, 30729-30737, see entire document	1-3, 7-10 ----- 4-6, 11-16

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/14696

## A. CLASSIFICATION OF SUBJECT MATTER: IPC (7):

C12N 15/54, 15/11, 15/63, 9/12, 1/21, 5/10, 15/09; C07K 16/40; C12Q 1/48